

A

Tue Apr 1 15:57:45 2003 [BLASTN 2.2.2 [Jan-08-2002], NCBI]  
 Repeats masked (summary below)  
 /home/glinda/vf/Legal/byeung/ss.DNA40370 (1650 bp)



Sequences producing High-scoring Segment Pairs:			Frame	Score	Match	Pct	E-val
1	P_AAF30502	Human PRO302 cDNA clone DNA40370-1217.	+	1650	1650	100	0.0
2	P_AAA13199	PRO302, vitellogenic carboxypeptidase h	+	1650	1650	100	0.0
3	P_AAX52258	Protein PRO302 cDNA clone DNA40370-1217	+	1650	1650	100	0.0
4	P_AAX25445	Human PRO216 cDNA clone UNQ265.	+	1650	1650	100	0.0
5	P_AAF72416	Human PRO302 cDNA.	+	1650	1650	100	0.0
6	P_ABL95586	Human angiogenesis related cDNA PRO302	+	1650	1650	100	0.0
7	P_ABL88097	Human PRO302 cDNA sequence SEQ ID NO:51	+	1650	1650	100	0.0
8	AX098272	Sequence 11 from Patent WO0119987. DNA	+	1650	1650	100	0.0
9	AX454466	Sequence 51 from Patent WO0208284. DNA	+	1650	1650	100	0.0
10	BD075577	Secretory and transmembrane polypeptide	+	1650	1650	100	0.0
11	BD173394	Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
12	BD173075	Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
13	AX490944	Sequence 51 from Patent WO0200690. DNA	+	1650	1650	100	0.0
14	BD172756	Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
15	BD172437	Secreted and transmembrane polypeptides	+	1650	1650	100	0.0
16	BD175428	Secretory and transmembrane polypeptide	+	1650	1650	100	0.0
17	P_ABV72656	Human retinoid inducible serine carboxy	+	1648	1648	100	0.0
18	P_ABV77921	Hypoxia-induced protein coding sequence	+	1640	1646	100	0.0
19	AF282618	Homo sapiens serine carboxypeptidase 1	+	1640	1646	100	0.0
20	NM_021626	Homo sapiens likely homolog of rat and	+	1640	1646	100	0.0
21	P_AAH15579	Human cDNA sequence SEQ ID NO:13881.	+	1637	1640	100	0.0
22	P_ABV28721	Human prostate expression marker cDNA 2	+	1637	1637	100	0.0
23	AK027373	Homo sapiens cDNA FLJ14467 fis, clone M	+	1637	1640	100	0.0
24	BD157571	Primer for synthesizing full-length cDN	+	1637	1640	100	0.0
25	P_AAH72787	Human cervical cancer marker nucleic ac	+	1633	1633	100	0.0
26	AX188369	Sequence 4064 from Patent WO0142467. D	+	1633	1633	100	0.0
27	P_AAD12590	Human protein having hydrophobic domain	+	1619	1622	100	0.0
28	AX191563	Sequence 85 from Patent WO0149728. DNA	+	1619	1622	100	0.0
29	AF113214	Homo sapiens MSTP034 mRNA, complete cds	+	1594	1594	100	0.0
30	P_AAC75884	Human ORFX ORF1439 polynucleotide seque	+	1543	1619	99	0.0
31	P_ABK30363	Human G-protein-coupled protease #133.	+	1407	1620	98	0.0
32	P_AAH89926	Human bone marrow cDNA, SEQ ID NO: 57.	+	1389	1577	97	0.0
33	AX191553	Sequence 75 from Patent WO0149728. DNA	+	1355	1358	100	0.0

>1 P\_AAF30502 Human PRO302 cDNA clone DNA40370-1217. cDNA, PAT 29-MAY-2001  
 (1650 bp) [1 seg]  
 Score = 1650 (3271 bits), Expect = 0.0  
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

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ss.DNA40370      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
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P_AAF30502      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****
P_AAF30502     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370    121 GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
P_AAF30502    121 GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370    181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
*****

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P_AAF30502	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG *****
P_AAF30502	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAAACCACTGGCTCCAGGCTGCC *****
P_AAF30502	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT *****
P_AAF30502	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC *****
P_AAF30502	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA *****
P_AAF30502	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC *****
P_AAF30502	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG *****
P_AAF30502	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
P_AAF30502	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
P_AAF30502	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC *****
P_AAF30502	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA *****
P_AAF30502	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
P_AAF30502	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC *****
P_AAF30502	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
P_AAF30502	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
P_AAF30502	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA *****
P_AAF30502	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTGAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
P_AAF30502	1201	GAACTGCCTAAATTGAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
P_AAF30502	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
P_AAF30502	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTGGGGGCACAGAGCT *****
P_AAF30502	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTGGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
P_AAF30502	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
P_AAF30502	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
P_AAF30502	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
P_AAF30502	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>2 P\_AAA13199 PRO302, vitellogenic carboxypeptidase homologue nucleotide sequence. (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
P_AAA13199	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
P_AAA13199	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
P_AAA13199	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

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*****
P_AAA13199      181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370     241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
*****
P_AAA13199      241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
ss.DNA40370     301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
*****
P_AAA13199      301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
ss.DNA40370     361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
*****
P_AAA13199      361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370     421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
*****
P_AAA13199      421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370     481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
*****
P_AAA13199      481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370     541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
*****
P_AAA13199      541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370     601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTGCGGTG
*****
P_AAA13199      601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTGCGGTG
ss.DNA40370     661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
*****
P_AAA13199      661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370     721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
*****
P_AAA13199      721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
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*****
P_AAA13199      781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370     841 TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
*****
P_AAA13199      841 TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370     901 CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
*****
P_AAA13199      901 CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370     961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
*****
P_AAA13199      961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370     1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
P_AAA13199      1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

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ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
		*****
P_AAA13199	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
		*****
P_AAA13199	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
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P_AAA13199	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
		*****
P_AAA13199	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
		*****
P_AAA13199	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
		*****
P_AAA13199	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
		*****
P_AAA13199	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
		*****
P_AAA13199	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
		*****
P_AAA13199	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA
		*****
P_AAA13199	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>3 P\_AAX52258 Protein PRO302 cDNA clone DNA40370-1217. DNA, PAT 25-JUN-1999  
(1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
		*****
P_AAX52258	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
		*****
P_AAX52258	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
		*****
P_AAX52258	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
P_AAX52258	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
P_AAX52258	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
P_AAX52258	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
P_AAX52258	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX52258	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
P_AAX52258	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
P_AAX52258	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCGGTG
P_AAX52258	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX52258	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX52258	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGGGGTGAACCTC
P_AAX52258	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX52258	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX52258	901	CAGAGCCACCTAGTTTGTCTTTGTTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
P_AAX52258	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

P_AAX52258	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
P_AAX52258	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA *****
P_AAX52258	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
P_AAX52258	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
P_AAX52258	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
P_AAX52258	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
P_AAX52258	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
P_AAX52258	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
P_AAX52258	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
P_AAX52258	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
P_AAX52258	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>4 P\_AAX25445 Human PRO216 cDNA clone UNQ265. (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
P_AAX25445	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
P_AAX25445	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
P_AAX25445	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTGGCC
P_AAX25445	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTGGCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
P_AAX25445	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAACACCTGGCTCCAGGCTGCC
P_AAX25445	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAACACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
P_AAX25445	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX25445	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
P_AAX25445	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
P_AAX25445	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCTGTTGATTCGGTG
P_AAX25445	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCTGTTGATTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX25445	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX25445	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAATTC
P_AAX25445	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAATTC
ss.DNA40370	841	TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX25445	841	TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX25445	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
P_AAX25445	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

P_AAX25445	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
P_AAX25445	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA *****
P_AAX25445	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
P_AAX25445	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
P_AAX25445	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
P_AAX25445	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
P_AAX25445	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
P_AAX25445	1441	GAGCTGAGGCCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
P_AAX25445	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
P_AAX25445	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
P_AAX25445	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>5 P\_AAF72416 Human PRO302 cDNA. (1650 bp) [1 seg]  
 Score = 1650 (3271 bits), Expect = 0.0  
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
P_AAF72416	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
P_AAF72416	61	GTCCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
P_AAF72416	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
P_AAF72416	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
		*****
P_AAF72416	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
		*****
P_AAF72416	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTTCAGTTATGTGAATGGTAGTGGT
		*****
P_AAF72416	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
P_AAF72416	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
		*****
P_AAF72416	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
		*****
P_AAF72416	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTTCGGTG
		*****
P_AAF72416	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
P_AAF72416	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
P_AAF72416	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
		*****
P_AAF72416	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTACACA
		*****
P_AAF72416	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTACACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
		*****
P_AAF72416	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
		*****
P_AAF72416	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
		*****

P_AAF72416	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
P_AAF72416	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA *****
P_AAF72416	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
P_AAF72416	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
P_AAF72416	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
P_AAF72416	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
P_AAF72416	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
P_AAF72416	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
P_AAF72416	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
P_AAF72416	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
P_AAF72416	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>6 P\_ABL95586 Human angiogenesis related cDNA PRO302 SEQ ID NO: 51. (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
P_ABL95586	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
P_ABL95586	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
P_ABL95586	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
P_ABL95586	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
		*****
P_ABL95586	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
		*****
P_ABL95586	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
		*****
P_ABL95586	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
P_ABL95586	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
		*****
P_ABL95586	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
		*****
P_ABL95586	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTGCGGTG
		*****
P_ABL95586	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCTGTTGATTGCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
P_ABL95586	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
P_ABL95586	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
		*****
P_ABL95586	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
		*****
P_ABL95586	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
		*****
P_ABL95586	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATCCTGAGGATCAATCC
		*****
P_ABL95586	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC



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*****
P_ABL95586      1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370     1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
P_ABL95586      1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370     1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
*****
P_ABL95586      1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370     1201 GAACTGCCTAAATTCAAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
P_ABL95586      1201 GAACTGCCTAAATTCAAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370     1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
P_ABL95586      1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370     1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
P_ABL95586      1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370     1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
P_ABL95586      1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370     1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
P_ABL95586      1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370     1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
P_ABL95586      1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370     1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
P_ABL95586      1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370     1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
P_ABL95586      1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>7 P\_ABL88097 Human PRO302 cDNA sequence SEQ ID NO:51. cDNA, PAT 16-MAY-2002 (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

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ss.DNA40370      1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
P_ABL88097       1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****
P_ABL88097      61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370     121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****

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P_ABL88097	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC *****
P_ABL88097	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG *****
P_ABL88097	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC *****
P_ABL88097	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT *****
P_ABL88097	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC *****
P_ABL88097	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA *****
P_ABL88097	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC *****
P_ABL88097	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG *****
P_ABL88097	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
P_ABL88097	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
P_ABL88097	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC *****
P_ABL88097	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAATAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTACACA *****
P_ABL88097	841	TATAACATCTTAATAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTACACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
P_ABL88097	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC *****
P_ABL88097	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
		*****
P_ABL88097	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
		*****
P_ABL88097	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA
		*****
P_ABL88097	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAAGTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
		*****
P_ABL88097	1201	GAAGTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
		*****
P_ABL88097	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
		*****
P_ABL88097	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
		*****
P_ABL88097	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
		*****
P_ABL88097	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
		*****
P_ABL88097	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
		*****
P_ABL88097	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA
		*****
P_ABL88097	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>8 AX098272 Sequence 11 from Patent WO0119987. DNA, linear, PAT 02-APR-2001  
(1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
		*****
AX098272	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
		*****
AX098272	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

		*****
AX098272	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
AX098272	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
		*****
AX098272	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
		*****
AX098272	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTCACTTATGTGAATGGTAGTGGT
		*****
AX098272	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACCTGGGTTCACTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
AX098272	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATATGGA
		*****
AX098272	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCATATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
		*****
AX098272	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
		*****
AX098272	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
AX098272	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
AX098272	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
		*****
AX098272	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
		*****
AX098272	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
		*****
AX098272	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
		*****
AX098272	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
		*****
AX098272	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
		*****
AX098272	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
		*****
AX098272	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAAGTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
		*****
AX098272	1201	GAAGTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
		*****
AX098272	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
		*****
AX098272	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
		*****
AX098272	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
		*****
AX098272	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
		*****
AX098272	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
		*****
AX098272	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA
		*****
AX098272	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>9 AX454466 Sequence 51 from Patent WO0208284. DNA, linear, PAT 06-JUL-2002  
 (1650 bp) [1 seg]  
 Score = 1650 (3271 bits), Expect = 0.0  
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
		*****
AX454466	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
		*****
AX454466	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
		*****
AX454466	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
AX454466	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
		*****
AX454466	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
		*****
AX454466	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
		*****
AX454466	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
AX454466	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
		*****
AX454466	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
		*****
AX454466	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
		*****
AX454466	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
AX454466	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
AX454466	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
		*****
AX454466	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
		*****
AX454466	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
		*****
AX454466	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
		*****

AX454466	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
AX454466	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
AX454466	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA *****
AX454466	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
AX454466	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
AX454466	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
AX454466	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
AX454466	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
AX454466	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
AX454466	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
AX454466	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
AX454466	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>10 BD075577 Secretory and transmembrane polypeptide and nucleic acid encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
BD075577	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
BD075577	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
		*****
BD075577	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
BD075577	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
		*****
BD075577	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
		*****
BD075577	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
		*****
BD075577	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
BD075577	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
		*****
BD075577	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
		*****
BD075577	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGCGTG
		*****
BD075577	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGCGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
BD075577	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
BD075577	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
		*****
BD075577	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
		*****
BD075577	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
		*****
BD075577	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAA AATTATTCCTGAGGATCAATCC



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*****
BD075577      961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370    1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD075577      1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370    1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD075577      1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370    1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA
*****
BD075577      1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370    1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCTAAATCTTTG
*****
BD075577      1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCTAAATCTTTG
ss.DNA40370    1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD075577      1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370    1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD075577      1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370    1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD075577      1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370    1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD075577      1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370    1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD075577      1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370    1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
BD075577      1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370    1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD075577      1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>11 BD173394 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

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ss.DNA40370    1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
BD173394       1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370    61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****

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BD173394	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
BD173394	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC *****
BD173394	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG *****
BD173394	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC *****
BD173394	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT *****
BD173394	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC *****
BD173394	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATATGGA *****
BD173394	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC *****
BD173394	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG *****
BD173394	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
BD173394	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
BD173394	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC *****
BD173394	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA *****
BD173394	841	TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
BD173394	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

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ss.DNA40370  961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCC
*****
BD173394     961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAATTTATTCCTGAGGATCAATCC

ss.DNA40370  1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD173394     1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370  1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD173394     1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370  1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
*****
BD173394     1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA

ss.DNA40370  1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTG
*****
BD173394     1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTG

ss.DNA40370  1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD173394     1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370  1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD173394     1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370  1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD173394     1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

ss.DNA40370  1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD173394     1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370  1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD173394     1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370  1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
BD173394     1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

ss.DNA40370  1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD173394     1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>12 BD173075 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

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ss.DNA40370  1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****
BD173075     1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370  61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

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		*****
BD173075	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
		*****
BD173075	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
BD173075	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
		*****
BD173075	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCC
		*****
BD173075	301	GAAATTGGGCCCCTTGACAGTGATCTCAAACACGGAACACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
		*****
BD173075	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
BD173075	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
		*****
BD173075	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
		*****
BD173075	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG
		*****
BD173075	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
BD173075	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
BD173075	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
		*****
BD173075	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAACATAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
		*****
BD173075	841	TATAACATCTTAACATAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
		*****
BD173075	901	CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
		*****
BD173075	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
		*****
BD173075	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
		*****
BD173075	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
		*****
BD173075	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
		*****
BD173075	1201	GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
		*****
BD173075	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
		*****
BD173075	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
		*****
BD173075	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
		*****
BD173075	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
		*****
BD173075	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
		*****
BD173075	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA
		*****
BD173075	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>13 AX490944 Sequence 51 from Patent WO0200690. DNA, linear, PAT 16-AUG-2002 (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
		*****
AX490944	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
		*****
AX490944	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
		*****
AX490944	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
AX490944	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
		*****
AX490944	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
		*****
AX490944	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
		*****
AX490944	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
AX490944	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
		*****
AX490944	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
		*****
AX490944	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
		*****
AX490944	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
AX490944	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
AX490944	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
		*****
AX490944	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370	841	TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
		*****
AX490944	841	TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
		*****

AX490944	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC *****
AX490944	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTGAGGATCAATCC
ss.DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
AX490944	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
AX490944	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA *****
AX490944	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
AX490944	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
AX490944	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
AX490944	1321	GGTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
AX490944	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
AX490944	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT *****
AX490944	1501	GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG *****
AX490944	1561	TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370	1621	ATCAAAATAAAGGATGATAATAGATATTAA *****
AX490944	1621	ATCAAAATAAAGGATGATAATAGATATTAA

>14 BD172756 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

ss.DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC *****
BD172756	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC

ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
		*****
BD172756	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
		*****
BD172756	121	GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
		*****
BD172756	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
		*****
BD172756	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
		*****
BD172756	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
		*****
BD172756	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
		*****
BD172756	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
		*****
BD172756	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
		*****
BD172756	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTGCGGTG
		*****
BD172756	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTGCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
		*****
BD172756	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
		*****
BD172756	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
		*****
BD172756	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
		*****
BD172756	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
ss.DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA



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*****
BD172756    901 CAGAGCCACCTAGTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
ss.DNA40370  961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
*****
BD172756    961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
ss.DNA40370  1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD172756    1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
ss.DNA40370  1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD172756    1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
ss.DNA40370  1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
*****
BD172756    1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCA
ss.DNA40370  1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
BD172756    1201 GAACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
ss.DNA40370  1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD172756    1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
ss.DNA40370  1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD172756    1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
ss.DNA40370  1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD172756    1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
ss.DNA40370  1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD172756    1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
ss.DNA40370  1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD172756    1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
ss.DNA40370  1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
BD172756    1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
ss.DNA40370  1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD172756    1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>15 BD172437 Secreted and transmembrane polypeptides and nucleic acids encoding (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

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ss.DNA40370    1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
*****

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BD172437	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT *****
BD172437	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC *****
BD172437	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC *****
BD172437	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG *****
BD172437	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAAACTTTGAG
ss.DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC *****
BD172437	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCC
ss.DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT *****
BD172437	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
ss.DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC *****
BD172437	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA *****
BD172437	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC *****
BD172437	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
ss.DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTCCGGTG *****
BD172437	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTCCGGTG
ss.DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
BD172437	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
BD172437	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC *****
BD172437	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
ss.DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTACACA *****
BD172437	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTACACA

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ss.DNA40370    901 CAGAGCCACCTAGTTTGTCTTTGTCTGAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
*****
BD172437      901 CAGAGCCACCTAGTTTGTCTTTGTCTGAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

ss.DNA40370    961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
*****
BD172437      961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

ss.DNA40370    1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD172437      1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370    1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD172437      1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370    1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA
*****
BD172437      1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGGCCA

ss.DNA40370    1201 GAACTGCCTAAATTCACTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
BD172437      1201 GAACTGCCTAAATTCACTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

ss.DNA40370    1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD172437      1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370    1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD172437      1321 GGTTCATATGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370    1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD172437      1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

ss.DNA40370    1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD172437      1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370    1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD172437      1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370    1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
BD172437      1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

ss.DNA40370    1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD172437      1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>16 BD175428 Secretory and transmembrane polypeptide and nucleic acid encoding (1650 bp) [1 seg]  
 Score = 1650 (3271 bits), Expect = 0.0  
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

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ss.DNA40370    1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

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*****
BD175428      1  GCCTGTTGCTGATGCTGCCGTGCGGTA CTGTGCATGGAGCTGGCACTGCGGCGCTCTCCC
ss.DNA40370   61  GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
*****
BD175428      61  GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
ss.DNA40370   121 GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
BD175428      121 GACTGGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
ss.DNA40370   181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
*****
BD175428      181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
ss.DNA40370   241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
*****
BD175428      241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
ss.DNA40370   301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
*****
BD175428      301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCC
ss.DNA40370   361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
*****
BD175428      361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGT
ss.DNA40370   421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
*****
BD175428      421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
ss.DNA40370   481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
*****
BD175428      481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGA
ss.DNA40370   541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
*****
BD175428      541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
ss.DNA40370   601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCGGTG
*****
BD175428      601 AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCGGTG
ss.DNA40370   661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
*****
BD175428      661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
ss.DNA40370   721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
*****
BD175428      721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
ss.DNA40370   781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
*****
BD175428      781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTC
ss.DNA40370   841 TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
*****
BD175428      841 TATAACATCTTAATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

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ss.DNA40370  901  CAGAGCCACCTAGTTTGTCTTTGTCTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
*****
BD175428    901  CAGAGCCACCTAGTTTGTCTTTGTCTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

ss.DNA40370  961  AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
*****
BD175428    961  AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

ss.DNA40370  1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
BD175428    1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

ss.DNA40370  1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
BD175428    1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG

ss.DNA40370  1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA
*****
BD175428    1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCA

ss.DNA40370  1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
BD175428    1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG

ss.DNA40370  1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
BD175428    1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

ss.DNA40370  1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
BD175428    1321 GGTCAATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

ss.DNA40370  1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
*****
BD175428    1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

ss.DNA40370  1441 GAGCTGAGGCCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
BD175428    1441 GAGCTGAGGCCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

ss.DNA40370  1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
BD175428    1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

ss.DNA40370  1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
BD175428    1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

ss.DNA40370  1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
BD175428    1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>17 P\_ABV72656 Human retinoid inducible serine carboxypeptidase cDNA. (1921 bp)  
[1 seg]

Score = 1648 (3267 bits), Expect = 0.0

Identities = 1648/1648 (100%), at 2,1-1649,1648, Strand +/+

ss.DNA40370	2	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
		*****
P_ABV72656	1	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
ss.DNA40370	62	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
		*****
P_ABV72656	61	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
ss.DNA40370	122	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
		*****
P_ABV72656	121	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
ss.DNA40370	182	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
		*****
P_ABV72656	181	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
ss.DNA40370	242	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
		*****
P_ABV72656	241	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
ss.DNA40370	302	AAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCA
		*****
P_ABV72656	301	AAATTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCA
ss.DNA40370	362	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTG
		*****
P_ABV72656	361	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTG
ss.DNA40370	422	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
		*****
P_ABV72656	421	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
ss.DNA40370	482	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
		*****
P_ABV72656	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
ss.DNA40370	542	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
		*****
P_ABV72656	541	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
ss.DNA40370	602	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTGC
		*****
P_ABV72656	601	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTGC
ss.DNA40370	662	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
		*****
P_ABV72656	661	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
ss.DNA40370	722	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
		*****
P_ABV72656	721	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
ss.DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCT
		*****
P_ABV72656	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACTTCT
ss.DNA40370	842	ATAACATCTTAACTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACAC
		*****

P_ABV72656	841	ATAACATCTTA	ACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
ss.DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA	*****
P_ABV72656	901	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA	
ss.DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT	*****
P_ABV72656	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT	
ss.DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA	*****
P_ABV72656	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA	
ss.DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC	*****
P_ABV72656	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC	
ss.DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAG	*****
P_ABV72656	1141	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAG	
ss.DNA40370	1202	AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG	*****
P_ABV72656	1201	AACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG	
ss.DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG	*****
P_ABV72656	1261	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG	
ss.DNA40370	1322	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC	*****
P_ABV72656	1321	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC	
ss.DNA40370	1382	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG	*****
P_ABV72656	1381	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG	
ss.DNA40370	1442	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG	*****
P_ABV72656	1441	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG	
ss.DNA40370	1502	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT	*****
P_ABV72656	1501	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT	
ss.DNA40370	1562	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA	*****
P_ABV72656	1561	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA	
ss.DNA40370	1622	TCAAAATAAAGGATGATAATAGATATTA	*****
P_ABV72656	1621	TCAAAATAAAGGATGATAATAGATATTA	

>18 P\_ABV77921 Hypoxia-induced protein coding sequence #35. DNA, PAT 12-NOV-2002 (1921 bp) [1 seg]

Score = 1640 (3251 bits), Expect = 0.0

Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/-

ss.DNA40370	2	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
		*****
P_ABV77921	1	CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
ss.DNA40370	62	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
		*****
P_ABV77921	61	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
ss.DNA40370	122	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
		*****
P_ABV77921	121	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
ss.DNA40370	182	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
		*****
P_ABV77921	181	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
ss.DNA40370	242	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
		*****
P_ABV77921	241	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
ss.DNA40370	302	AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCCA
		*****
P_ABV77921	301	AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCCA
ss.DNA40370	362	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTG
		*****
P_ABV77921	361	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTG
ss.DNA40370	422	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
		*****
P_ABV77921	421	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
ss.DNA40370	482	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
		*****
P_ABV77921	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
ss.DNA40370	542	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATCA
		*****
P_ABV77921	541	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATCA
ss.DNA40370	602	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCCTGTTGATTCCGTGC
		***** ** *****
P_ABV77921	601	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCCTGTTGATTCCGTGC
ss.DNA40370	662	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
		*****
P_ABV77921	661	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
ss.DNA40370	722	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
		*****
P_ABV77921	721	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
ss.DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
		*****
P_ABV77921	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
ss.DNA40370	842	ATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGCTAGAATTCACAC



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*****
P_ABV77921      841 ATAACATCTTAACTAAAAGCACTCCACGCTACAATGGAGTCGAGTCTAGAATTCACAC
ss.DNA40370     902 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
*****
P_ABV77921      901 AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
ss.DNA40370     962 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
*****
P_ABV77921      961 GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
ss.DNA40370    1022 GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
*****
P_ABV77921    1021 GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
ss.DNA40370    1082 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
*****
P_ABV77921    1081 TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
ss.DNA40370    1142 TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAG
*****
P_ABV77921    1141 TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAG
ss.DNA40370    1202 AACTGCCTAAATTCTAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
*****
P_ABV77921    1201 AACTGCCTAAATTCTAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
ss.DNA40370    1262 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
*****
P_ABV77921    1261 AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
ss.DNA40370    1322 GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
*****
P_ABV77921    1321 GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
ss.DNA40370    1382 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
*****
P_ABV77921    1381 AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
ss.DNA40370    1442 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
*****
P_ABV77921    1441 AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
ss.DNA40370    1502 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
*****
P_ABV77921    1501 ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
ss.DNA40370    1562 GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA
*****
P_ABV77921    1561 GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA
ss.DNA40370    1622 TCAAAAATAAAGGATGATAATAGATATTA
*****
P_ABV77921    1621 TCAAAAATAAAGGATGATAATAGATATTA

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>19 AF282618 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)  
(1921 bp) [1 seg]  
Score = 1640 (3251 bits), Expect = 0.0

Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+

```
ss.DNA40370      2 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
*****
AF282618         1 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG

ss.DNA40370     62 TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
*****
AF282618        61 TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG

ss.DNA40370    122 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
*****
AF282618     121 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT

ss.DNA40370    182 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
*****
AF282618     181 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC

ss.DNA40370    242 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGG
*****
AF282618     241 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGG

ss.DNA40370    302 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCA
*****
AF282618     301 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCA

ss.DNA40370    362 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTG
*****
AF282618     361 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTG

ss.DNA40370    422 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
*****
AF282618     421 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT

ss.DNA40370    482 TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG
*****
AF282618     481 TCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAG

ss.DNA40370    542 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCA
*****
AF282618     541 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCA

ss.DNA40370    602 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCCTGTTGATTGGTG
***** ** *****
AF282618     601 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGGATCTCCCCCTGTTGATTGGTG

ss.DNA40370    662 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
*****
AF282618     661 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG

ss.DNA40370    722 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
*****
AF282618     721 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA

ss.DNA40370    782 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAATTCT
*****
AF282618     781 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAATTCT
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ss.DNA40370	842	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
		*****
AF282618	841	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
ss.DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
		*****
AF282618	901	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
ss.DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
		*****
AF282618	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
ss.DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
		*****
AF282618	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
ss.DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
		*****
AF282618	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
ss.DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
		*****
AF282618	1141	TGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
ss.DNA40370	1202	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
		*****
AF282618	1201	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
ss.DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
		*****
AF282618	1261	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
ss.DNA40370	1322	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
		*****
AF282618	1321	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
ss.DNA40370	1382	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
		*****
AF282618	1381	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
ss.DNA40370	1442	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
		*****
AF282618	1441	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
ss.DNA40370	1502	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
		*****
AF282618	1501	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
ss.DNA40370	1562	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA
		*****
AF282618	1561	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGA
ss.DNA40370	1622	TCAAAATAAAGGATGATAATAGATATTA
		*****
AF282618	1621	TCAAAATAAAGGATGATAATAGATATTA

>20 NM\_021626 Homo sapiens likely homolog of rat and mouse retinoid-inducible (1921 bp) [1 seg]

Score = 1640 (3251 bits), Expect = 0.0  
Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+

```
ss.DNA40370      2 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
   NM_021626      1 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG

ss.DNA40370     62 TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
   NM_021626     61 TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG

ss.DNA40370    122 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
   NM_021626    121 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT

ss.DNA40370    182 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
   NM_021626    181 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC

ss.DNA40370    242 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACCTTTGAGG
   NM_021626    241 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACCTTTGAGG

ss.DNA40370    302 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCA
   NM_021626    301 AAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCA

ss.DNA40370    362 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTG
   NM_021626    361 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTG

ss.DNA40370    422 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
   NM_021626    421 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT

ss.DNA40370    482 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAG
   NM_021626    481 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAG

ss.DNA40370    542 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
   NM_021626    541 GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA

ss.DNA40370    602 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCCTGTTGATTGCGTGC
   NM_021626    601 AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCCTGTTGATTGCGTGC

ss.DNA40370    662 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
   NM_021626    661 TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG

ss.DNA40370    722 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
   NM_021626    721 TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA

ss.DNA40370    782 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
   NM_021626    781 CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
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ss.DNA40370	842	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
		*****
NM_021626	841	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
ss.DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
		*****
NM_021626	901	AGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
ss.DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
		*****
NM_021626	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
ss.DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
		*****
NM_021626	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
ss.DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
		*****
NM_021626	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
ss.DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCAG
		*****
NM_021626	1141	TGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAACTGAAGTGGCCAG
ss.DNA40370	1202	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
		*****
NM_021626	1201	AACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
ss.DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
		*****
NM_021626	1261	AAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTG
ss.DNA40370	1322	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
		*****
NM_021626	1321	GTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
ss.DNA40370	1382	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
		*****
NM_021626	1381	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
ss.DNA40370	1442	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
		*****
NM_021626	1441	AGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
ss.DNA40370	1502	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
		*****
NM_021626	1501	ATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTT
ss.DNA40370	1562	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA
		*****
NM_021626	1561	GGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTTTTGA
ss.DNA40370	1622	TCAAAATAAAGGATGATAATAGATATTA
		*****
NM_021626	1621	TCAAAATAAAGGATGATAATAGATATTA

>21 P\_AAH15579 Human cDNA sequence SEQ ID NO:13881. (1641 bp) [1 seg]

Score = 1637 (3245 bits), Expect = 0.0  
Identities = 1640/1641 (99%), at 8,1-1648,1641, Strand +/+

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ss.DNA40370      8 GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
*****
P_AAH15579       1 GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

ss.DNA40370     68 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
*****
P_AAH15579     61 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC

ss.DNA40370    128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
*****
P_AAH15579    121 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT

ss.DNA40370    188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA
*****
P_AAH15579    181 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA

ss.DNA40370    248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
*****
P_AAH15579    241 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG

ss.DNA40370    308 GGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCC
*****
P_AAH15579    301 GGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCC

ss.DNA40370    368 TATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCCTATG
*****
P_AAH15579    361 TATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCCTATG

ss.DNA40370    428 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
*****
P_AAH15579    421 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370    488 GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
*****
P_AAH15579    481 GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA

ss.DNA40370    548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
*****
P_AAH15579    541 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370    608 ACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTGGTGCTCTCCT
*****
P_AAH15579    601 ACTTTGCGGGGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTGGTGCTCTCCT

ss.DNA40370    668 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
*****
P_AAH15579    661 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA

ss.DNA40370    728 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
*****
P_AAH15579    721 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC

ss.DNA40370    788 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
*****
P_AAH15579    781 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
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ss.DNA40370	848	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
P_AAH15579	841	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
ss.DNA40370	908	ACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
P_AAH15579	901	ACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
ss.DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
P_AAH15579	961	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
ss.DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
P_AAH15579	1021	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
ss.DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
P_AAH15579	1081	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
ss.DNA40370	1148	TCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC
P_AAH15579	1141	TCATCGTAGATACCATGGGTGAGGAGGCTGGGTGCGGAAACTGAAGTGGCCAGAACTGC
ss.DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
P_AAH15579	1201	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
ss.DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
P_AAH15579	1261	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
ss.DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
P_AAH15579	1321	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
ss.DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
P_AAH15579	1381	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
ss.DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
P_AAH15579	1441	GGCCGCTGAAGCTGTAGGAAGCGCCACTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
ss.DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT
P_AAH15579	1501	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT
ss.DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
P_AAH15579	1561	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
ss.DNA40370	1628	TAAAGGATGATAATAGATATT
P_AAH15579	1621	TAAAGGATGATAATAGATATT

>22 P\_ABV28721 Human prostate expression marker cDNA 28712. (1973 bp) [1 seg]

Score = 1637 (3245 bits), Expect = 0.0  
Identities = 1637/1637 (100%), at 13,32-1649,1668, Strand +/-

ss.DNA40370	13	TGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGG
		*****
P_ABV28721	32	TGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGG
ss.DNA40370	73	TTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCACA
		*****
P_ABV28721	92	TTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCACA
ss.DNA40370	133	GAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG
		*****
P_ABV28721	152	GAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG
ss.DNA40370	193	TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGG
		*****
P_ABV28721	212	TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGG
ss.DNA40370	253	CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGGAGAAATTGGGCCC
		*****
P_ABV28721	272	CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGGAGAAATTGGGCCC
ss.DNA40370	313	CTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
		*****
P_ABV28721	332	CTTGACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
ss.DNA40370	373	GTGGATAATCCCGTGGGCACTGGGTTTCAAGTATGTGAATGGTAGTGGTGCCTATGCCAAG
		*****
P_ABV28721	392	GTGGATAATCCCGTGGGCACTGGGTTTCAAGTATGTGAATGGTAGTGGTGCCTATGCCAAG
ss.DNA40370	433	GACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCAC
		*****
P_ABV28721	452	GACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCAC
ss.DNA40370	493	AAAGAATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCA
		*****
P_ABV28721	512	AAAGAATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCA
ss.DNA40370	553	GCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTT
		*****
P_ABV28721	572	GCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTT
ss.DNA40370	613	GCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCTGTTGATTTCGGTGCTCTCCTGGGGA
		*****
P_ABV28721	632	GCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCTGTTGATTTCGGTGCTCTCCTGGGGA
ss.DNA40370	673	CCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTT
		*****
P_ABV28721	692	CCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTT
ss.DNA40370	733	GCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGG
		*****
P_ABV28721	752	GCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGG
ss.DNA40370	793	GGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTA
		*****
P_ABV28721	812	GGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTA



ss.DNA40370	853	ACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTA *****
P_ABV28721	872	ACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTA
ss.DNA40370	913	GTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATG *****
P_ABV28721	932	GTTTGTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATG
ss.DNA40370	973	AATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAG *****
P_ABV28721	992	AATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAG
ss.DNA40370	1033	GCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTG *****
P_ABV28721	1052	GCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTG
ss.DNA40370	1093	GACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATC *****
P_ABV28721	1112	GACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATC
ss.DNA40370	1153	GTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAA *****
P_ABV28721	1172	GTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAA
ss.DNA40370	1213	TTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCCT *****
P_ABV28721	1232	TTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCCT
ss.DNA40370	1273	TTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTT *****
P_ABV28721	1292	TTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTT
ss.DNA40370	1333	CCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG *****
P_ABV28721	1352	CCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG
ss.DNA40370	1393	GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCG *****
P_ABV28721	1412	GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCG
ss.DNA40370	1453	CTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGT *****
P_ABV28721	1472	CTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGT
ss.DNA40370	1513	TCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTT *****
P_ABV28721	1532	TCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTT
ss.DNA40370	1573	CTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAG *****
P_ABV28721	1592	CTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAG
ss.DNA40370	1633	GATGATAATAGATATTA *****
P_ABV28721	1652	GATGATAATAGATATTA

>23 AK027373 Homo sapiens cDNA FLJ14467 fis, clone MAMMA1000672, weakly (1641 bp) [1 seg]

Score = 1637 (3245 bits), Expect = 0.0

Identities = 1640/1641 (99%), at 8,1-1648,1641, Strand +/+

```
ss.DNA40370      8 GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
   AK027373      1 GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

ss.DNA40370     68 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
   AK027373     61 GGTGGTTGCTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC

ss.DNA40370    128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
   AK027373    121 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT

ss.DNA40370    188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA
   AK027373    181 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCA

ss.DNA40370    248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
   AK027373    241 TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG

ss.DNA40370    308 GGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCC
   AK027373    301 GGCCCCCTTGACAGTGATCTCAAACCACGAAAACCACTGGCTCCAGGCTGCCAGTCTCC

ss.DNA40370    368 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATG
   AK027373    361 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTGCCTATG

ss.DNA40370    428 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
   AK027373    421 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370    488 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
   AK027373    481 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA

ss.DNA40370    548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
   AK027373    541 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370    608 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT
   AK027373    601 ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT

ss.DNA40370    668 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
   AK027373    661 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA

ss.DNA40370    728 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
   AK027373    721 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC

ss.DNA40370    788 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
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		*****
AK027373	781	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACA
ss.DNA40370	848	TCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
		*****
AK027373	841	TCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
ss.DNA40370	908	ACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
		*****
AK027373	901	ACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
ss.DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
		*****
AK027373	961	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
ss.DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
		*****
AK027373	1021	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
ss.DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
		*****
AK027373	1081	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
ss.DNA40370	1148	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAACTGC
		*****
AK027373	1141	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAACTGC
ss.DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
		*****
AK027373	1201	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
ss.DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
		*****
AK027373	1261	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
ss.DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
		*****
AK027373	1321	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
ss.DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
		*****
AK027373	1381	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
ss.DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
		*****
AK027373	1441	GGCCGCTGAAGCTGTAGGAAGCGCCACTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
ss.DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
		*****
AK027373	1501	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
ss.DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTGTATCAAAA
		*****
AK027373	1561	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTGTATCAAAA
ss.DNA40370	1628	TAAAGGATGATAATAGATATT
		*****
AK027373	1621	TAAAGGATGATAATAGATATT

>24 BD157571 Primer for synthesizing full-length cDNA and use thereof. (1641 bp)  
[1 seg]

Score = 1637 (3245 bits), Expect = 0.0

Identities = 1640/1641 (99%), at 8,1-1648,1641, Strand +/-

```
ss.DNA40370      8  GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
      *****
BD157571         1  GCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC

ss.DNA40370     68  GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
      *****
BD157571        61  GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC

ss.DNA40370    128  CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
      *****
BD157571       121  CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT

ss.DNA40370    188  TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
      *****
BD157571       181  TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA

ss.DNA40370    248  TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTG
      *****
BD157571       241  TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTG

ss.DNA40370    308  GGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCC
      *****
BD157571       301  GGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCC

ss.DNA40370    368  TATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCCTATG
      *****
BD157571       361  TATTTGTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCCTATG

ss.DNA40370    428  CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
      *****
BD157571       421  CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT

ss.DNA40370    488  GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
      *****
BD157571       481  GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA

ss.DNA40370    548  TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
      *****
BD157571       541  TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA

ss.DNA40370    608  ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT
      *****
BD157571       601  ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT

ss.DNA40370    668  GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
      *****
BD157571       661  GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA

ss.DNA40370    728  AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
      *****
BD157571       721  AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
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ss.DNA40370	788	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAGTCTCTATAACA
		*****
BD157571	781	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAGTCTCTATAACA
ss.DNA40370	848	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
		*****
BD157571	841	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
ss.DNA40370	908	ACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
		*****
BD157571	901	ACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
ss.DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAATTATTCTGAGGATCAATCCTGGGGAG
		*****
BD157571	961	TCATGAATGGCCCCATCAGAAAGAAGCTCAAATTATTCTGAGGATCAATCCTGGGGAG
ss.DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
		*****
BD157571	1021	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
ss.DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
		*****
BD157571	1081	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
ss.DNA40370	1148	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGC
		*****
BD157571	1141	TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGC
ss.DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
		*****
BD157571	1201	CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
ss.DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
		*****
BD157571	1261	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
ss.DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
		*****
BD157571	1321	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
ss.DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
		*****
BD157571	1381	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
ss.DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
		*****
BD157571	1441	GGCCGCTGAAGCTGTAGGAAGCGCCACTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
ss.DNA40370	1508	AAGGTTCTGACCAGCTTCTGTCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
		*****
BD157571	1501	AAGGTTCTGACCAGCTTCTGTCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
ss.DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
		*****
BD157571	1561	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
ss.DNA40370	1628	TAAAGGATGATAATAGATATT
		*****

BD157571 1621 TAAAGGATGATAATAGATATT

>25 P\_AAH72787 Human cervical cancer marker nucleic acid 4061. (1977 bp) [1 seg]  
Score = 1633 (3237 bits), Expect = 0.0  
Identities = 1633/1633 (100%), at 17,40-1649,1672, Strand +/-

ss.DNA40370	17	GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGC
		*****
P_AAH72787	40	GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGC
ss.DNA40370	77	TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGG
		*****
P_AAH72787	100	TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGG
ss.DNA40370	137	AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC
		*****
P_AAH72787	160	AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC
ss.DNA40370	197	TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTC
		*****
P_AAH72787	220	TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTC
ss.DNA40370	257	AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGGAAATTGGGCCCTTG
		*****
P_AAH72787	280	AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGGAAATTGGGCCCTTG
ss.DNA40370	317	ACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG
		*****
P_AAH72787	340	ACAGTGATCTCAAACCACGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG
ss.DNA40370	377	ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC
		*****
P_AAH72787	400	ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC
ss.DNA40370	437	TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
		*****
P_AAH72787	460	TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
ss.DNA40370	497	AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG
		*****
P_AAH72787	520	AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG
ss.DNA40370	557	GCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGG
		*****
P_AAH72787	580	GCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGG
ss.DNA40370	617	GGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCTGGGGACCTT
		*****
P_AAH72787	640	GGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCTGGGGACCTT
ss.DNA40370	677	ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG
		*****
P_AAH72787	700	ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG
ss.DNA40370	737	AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA
		*****
P_AAH72787	760	AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA

ss.DNA40370	797	AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA *****
P_AAH72787	820	AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA
ss.DNA40370	857	AAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTT *****
P_AAH72787	880	AAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTT
ss.DNA40370	917	GTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG *****
P_AAH72787	940	GTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG
ss.DNA40370	977	GCCCCATCAGAAAAGAAGCTCAAAATTATTCTCTGAGGATCAATCCTGGGGAGGCCAGGCTA *****
P_AAH72787	1000	GCCCCATCAGAAAAGAAGCTCAAAATTATTCTCTGAGGATCAATCCTGGGGAGGCCAGGCTA
ss.DNA40370	1037	CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG *****
P_AAH72787	1060	CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG
ss.DNA40370	1097	AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG *****
P_AAH72787	1120	AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG
ss.DNA40370	1157	ATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCA *****
P_AAH72787	1180	ATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCA
ss.DNA40370	1217	GTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG *****
P_AAH72787	1240	GTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG
ss.DNA40370	1277	TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTT *****
P_AAH72787	1300	TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTT
ss.DNA40370	1337	CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATG *****
P_AAH72787	1360	CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATG
ss.DNA40370	1397	GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA *****
P_AAH72787	1420	GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA
ss.DNA40370	1457	AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG *****
P_AAH72787	1480	AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG
ss.DNA40370	1517	ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC *****
P_AAH72787	1540	ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC
ss.DNA40370	1577	TTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG *****
P_AAH72787	1600	TTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG
ss.DNA40370	1637	ATAATAGATATTA *****

P\_AAH72787 1660 ATAATAGATATTA

>26 AX188369 Sequence 4064 from Patent WO0142467. DNA, linear, PAT 06-AUG-2001 (1977 bp) [1 seg]

Score = 1633 (3237 bits), Expect = 0.0

Identities = 1633/1633 (100%), at 17,40-1649,1672, Strand +/-

```
ss.DNA40370 17 GCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCGCGGTGGTTGC
*****
AX188369 40 GCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCGCGGTGGTTGC

ss.DNA40370 77 TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCACAGAGG
*****
AX188369 100 TGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCCACAGAGG

ss.DNA40370 137 AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC
*****
AX188369 160 AGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGC

ss.DNA40370 197 TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTC
*****
AX188369 220 TCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTC

ss.DNA40370 257 AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCCCTTG
*****
AX188369 280 AGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGCCCCCTTG

ss.DNA40370 317 ACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG
*****
AX188369 340 ACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGG

ss.DNA40370 377 ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC
*****
AX188369 400 ATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACC

ss.DNA40370 437 TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
*****
AX188369 460 TGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG

ss.DNA40370 497 AATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG
*****
AX188369 520 AATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTG

ss.DNA40370 557 GCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGG
*****
AX188369 580 GCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCAACTTTGCGG

ss.DNA40370 617 GGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTGCGTGCTCTCCTGGGGACCTT
*****
AX188369 640 GGGTTGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTGCGTGCTCTCCTGGGGACCTT

ss.DNA40370 677 ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG
*****
AX188369 700 ACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAG

ss.DNA40370 737 AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA
*****
AX188369 760 AGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGA
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ss.DNA40370	797	AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA *****
AX188369	820	AAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACTA
ss.DNA40370	857	AAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTT *****
AX188369	880	AAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTT
ss.DNA40370	917	GTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG *****
AX188369	940	GTCTTTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATG
ss.DNA40370	977	GCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTA *****
AX188369	1000	GCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTA
ss.DNA40370	1037	CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG *****
AX188369	1060	CCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACG
ss.DNA40370	1097	AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG *****
AX188369	1120	AGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAG
ss.DNA40370	1157	ATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCA *****
AX188369	1180	ATACCATGGGTCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCA
ss.DNA40370	1217	GTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG *****
AX188369	1240	GTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTG
ss.DNA40370	1277	TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTT *****
AX188369	1300	TCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTT
ss.DNA40370	1337	CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGAAGTCAAGCAAGATAGGATG *****
AX188369	1360	CTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGAAGTCAAGCAAGATAGGATG
ss.DNA40370	1397	GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA *****
AX188369	1420	GATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGA
ss.DNA40370	1457	AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG *****
AX188369	1480	AGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTG
ss.DNA40370	1517	ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC *****
AX188369	1540	ACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGC
ss.DNA40370	1577	TTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG *****
AX188369	1600	TTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATG
ss.DNA40370	1637	ATAATAGATATTA

\*\*\*\*\*  
AX188369 1660 ATAATAGATATTA

>27 P\_AAD12590 Human protein having hydrophobic domain encoding cDNA clone  
HP03959. (1897 bp) [1 seg]

Score = 1619 (3209 bits), Expect = 0.0

Identities = 1622/1623 (99%), at 27,1-1649,1623, Strand +/-

```
ss.DNA40370      27  ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCC GCGGTGGTTGCTGCTGCTGCC
*****
P_AAD12590       1  ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCC GCGGTGGTTGCTGCTGCTGCC

ss.DNA40370      87  GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCC CACAGAGGAGGGCAAGGA
*****
P_AAD12590       61  GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCC CACAGAGGAGGGCAAGGA

ss.DNA40370     147  AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTT CTGGTGGCTCTATTATGC
*****
P_AAD12590     121  AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTT CTGGTGGCTCTATTATGC

ss.DNA40370     207  CACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCAT GTGGCTTCAGGGCGGTCC
*****
P_AAD12590     181  CACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCAT GTGGCTTCAGGGCGGTCC

ss.DNA40370     267  AGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGG CCCCCTTGACAGTGATCT
*****
P_AAD12590     241  AGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGG CCCCCTTGACAGTGATCT

ss.DNA40370     327  CAAACCACGGA AAAACCACTGGCTCCAGGCTGCCAGTCTCCT ATTTGTGGATAATCCCGT
*****
P_AAD12590     301  CAAACCACGGA AAAACCACTGGCTCCAGGCTGCCAGTCTCCT ATTTGTGGATAATCCCGT

ss.DNA40370     387  GGGCACTGGGTT CAGTTATGTGAATGGTAGTGGTGCCTATGCCA AGGACCTGGCTATGGT
*****
P_AAD12590     361  GGGCACTGGGTT CAGTTATGTGAATGGTAGTGGTGCCTATGCCA AGGACCTGGCTATGGT

ss.DNA40370     447  GGCTTCAGACAT GATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACA AAGAATTCCAGAC
*****
P_AAD12590     421  GGCTTCAGACAT GATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACA AAGAATTCCAGAC

ss.DNA40370     507  AGTTCCATTCTA CATTCTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC ATTTGGTCT
*****
P_AAD12590     481  AGTTCCATTCTA CATTCTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC ATTTGGTCT

ss.DNA40370     567  AGAGCTTTATAA GGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGG GGTGCCTT
*****
P_AAD12590     541  AGAGCTTTATAA GGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGG GGTGCCTT

ss.DNA40370     627  GGGTGATTCTTG GATCTCCCCTGTTGATTGCGTGCTCTCCTGGGGACCTTACC TGTACAG
*****
P_AAD12590     601  GGGTGATTCTTG GATCTCCCCTGTTGATTGCGTGCTCTCCTGGGGACCTTACC TGTACAG

ss.DNA40370     687  CATGTCTCTTCT CGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAG CAAGTACT
*****
P_AAD12590     661  CATGTCTCTTCT CGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAG CAAGTACT

ss.DNA40370     747  GAATGCCGTAAAT AAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGC AGAAAT
*****
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P_AAD12590	721	GAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
ss.DNA40370	807	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCC *****
P_AAD12590	781	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCC
ss.DNA40370	867	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA *****
P_AAD12590	841	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA
ss.DNA40370	927	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG *****
P_AAD12590	901	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG
ss.DNA40370	987	AAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT *****
P_AAD12590	961	AAAGAAGCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT
ss.DNA40370	1047	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA *****
P_AAD12590	1021	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA
ss.DNA40370	1107	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG *****
P_AAD12590	1081	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG
ss.DNA40370	1167	TCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAA *****
P_AAD12590	1141	TCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAA
ss.DNA40370	1227	GTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTA *****
P_AAD12590	1201	GTGGAAGGCCCTGTACAGTGACCCTAAATCTCTGGAACATCTGCTTTTGTCAAGTCCTA
ss.DNA40370	1287	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGG *****
P_AAD12590	1261	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGG
ss.DNA40370	1347	GGACATGGCTCTGAAGATGATGAGACTGGTGAAGTCAAGCAAGATAGGATGGATGGGGCTG *****
P_AAD12590	1321	GGACATGGCTCTGAAGATGATGAGACTGGTGAAGTCAAGCAAGATAGGATGGATGGGGCTG
ss.DNA40370	1407	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA *****
P_AAD12590	1381	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA
ss.DNA40370	1467	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT *****
P_AAD12590	1441	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT
ss.DNA40370	1527	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA *****
P_AAD12590	1501	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA
ss.DNA40370	1587	AACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATA *****
P_AAD12590	1561	AACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATA

ss.DNA40370 1647 TTA  
\*\*\*  
P\_AAD12590 1621 TTA

>28 AX191563 Sequence 85 from Patent WO0149728. DNA, linear, PAT 15-AUG-2001  
(1897 bp) [1 seg]

Score = 1619 (3209 bits), Expect = 0.0

Identities = 1622/1623 (99%), at 27,1-1649,1623, Strand +/-

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ss.DNA40370 27 ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCC
*****
AX191563 1 ACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCC

ss.DNA40370 87 GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGA
*****
AX191563 61 GCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAGGAGGGCAAGGA

ss.DNA40370 147 AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGC
*****
AX191563 121 AGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGC

ss.DNA40370 207 CACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCC
*****
AX191563 181 CACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCC

ss.DNA40370 267 AGGCGGTTCTAGCACTGGATTTGGAACCTTTGAGGAAATTGGGCCCCCTTGACAGTGATCT
*****
AX191563 241 AGGCGGTTCTAGCACTGGATTTGGAACCTTTGAGGAAATTGGGCCCCCTTGACAGTGATCT

ss.DNA40370 327 CAAACCACGGAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGT
*****
AX191563 301 CAAACCACGGAACACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGT

ss.DNA40370 387 GGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGT
*****
AX191563 361 GGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGT

ss.DNA40370 447 GGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC
*****
AX191563 421 GGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC

ss.DNA40370 507 AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT
*****
AX191563 481 AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCT

ss.DNA40370 567 AGAGCTTTATAAGGCCATTACGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTT
*****
AX191563 541 AGAGCTTTATAAGGCCATTACGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTT

ss.DNA40370 627 GGGTGATTCTTGGATCTCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGTACAG
*****
AX191563 601 GGGTGATTCTTGGATCTCCCTGTTGATTGCGGTGCTCTCCTGGGGACCTTACCTGTACAG

ss.DNA40370 687 CATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACT
*****
AX191563 661 CATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACT

ss.DNA40370 747 GAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
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		*****
AX191563	721	GAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAAGCAGAAAT
ss.DNA40370	807	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCC
		*****
AX191563	781	GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCC
ss.DNA40370	867	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA
		*****
AX191563	841	CACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCA
ss.DNA40370	927	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG
		*****
AX191563	901	GCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAG
ss.DNA40370	987	AAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT
		*****
AX191563	961	AAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTT
ss.DNA40370	1047	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA
		*****
AX191563	1021	TGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGA
ss.DNA40370	1107	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG
		*****
AX191563	1081	GGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGG
ss.DNA40370	1167	TCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAA
		*****
AX191563	1141	TCAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGCTGAA
ss.DNA40370	1227	GTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTA
		*****
AX191563	1201	GTGGAAGGCCCTGTACAGTGACCCTAAATCTCTGGAACATCTGCTTTTGTCAAGTCCTA
ss.DNA40370	1287	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGG
		*****
AX191563	1261	CAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGG
ss.DNA40370	1347	GGACATGGCTCTGAAGATGATGAGACTGGTGAAGTCAAGCAAGATAGGATGGATGGGGCTG
		*****
AX191563	1321	GGACATGGCTCTGAAGATGATGAGACTGGTGAAGTCAAGCAAGATAGGATGGATGGGGCTG
ss.DNA40370	1407	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA
		*****
AX191563	1381	GAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGA
ss.DNA40370	1467	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT
		*****
AX191563	1441	AGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCT
ss.DNA40370	1527	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA
		*****
AX191563	1501	GCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAA
ss.DNA40370	1587	AACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATA
		*****
AX191563	1561	AACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAATAAAGGATGATAATAGATA

ss.DNA40370 1647 TTA  
\*\*\*  
AX191563 1621 TTA

>29 AF113214 Homo sapiens MSTP034 mRNA, complete cds. (1902 bp) [1 seg]  
Score = 1594 (3160 bits), Expect = 0.0  
Identities = 1594/1594 (100%), at 56,1-1649,1594, Strand +/+

ss.DNA40370 56 CTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTG  
\*\*\*\*\*  
AF113214 1 CTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTG

ss.DNA40370 116 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG  
\*\*\*\*\*  
AF113214 61 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG

ss.DNA40370 176 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC  
\*\*\*\*\*  
AF113214 121 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC

ss.DNA40370 236 TGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGT  
\*\*\*\*\*  
AF113214 181 TGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAGT

ss.DNA40370 296 TTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGG  
\*\*\*\*\*  
AF113214 241 TTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGG

ss.DNA40370 356 CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTA  
\*\*\*\*\*  
AF113214 301 CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTA

ss.DNA40370 416 GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA  
\*\*\*\*\*  
AF113214 361 GTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA

ss.DNA40370 476 CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT  
\*\*\*\*\*  
AF113214 421 CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT

ss.DNA40370 536 ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGA  
\*\*\*\*\*  
AF113214 481 ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGA

ss.DNA40370 596 CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATT  
\*\*\*\*\*  
AF113214 541 CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCTGGATCTCCCCTGTTGATT

ss.DNA40370 656 CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG  
\*\*\*\*\*  
AF113214 601 CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG

ss.DNA40370 716 CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG  
\*\*\*\*\*  
AF113214 661 CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG

ss.DNA40370 776 AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA

```

*****
AF113214      721 AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA
ss.DNA40370   836 ACTTCTATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAAT
*****
AF113214      781 ACTTCTATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAAT
ss.DNA40370   896 TCACACAGAGCCACCTAGTTTGTCTTTGTCTGTCAGCGCCACGTGAGACACCTACAACGAGATG
*****
AF113214      841 TCACACAGAGCCACCTAGTTTGTCTTTGTCTGTCAGCGCCACGTGAGACACCTACAACGAGATG
ss.DNA40370   956 CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATC
*****
AF113214      901 CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATC
ss.DNA40370   1016 AATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
*****
AF113214      961 AATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
ss.DNA40370   1076 CAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
*****
AF113214      1021 CAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
ss.DNA40370   1136 GACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGT
*****
AF113214      1081 GACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGT
ss.DNA40370   1196 GGCCAGAAGTGCCTAAATTAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAAT
*****
AF113214      1141 GGCCAGAAGTGCCTAAATTAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAAT
ss.DNA40370   1256 CTTTGGAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGA
*****
AF113214      1201 CTTTGGAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGA
ss.DNA40370   1316 AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
*****
AF113214      1261 AAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
ss.DNA40370   1376 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
*****
AF113214      1321 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
ss.DNA40370   1436 GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
*****
AF113214      1381 GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
ss.DNA40370   1496 GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
*****
AF113214      1441 GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
ss.DNA40370   1556 CAATTTGGAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTG
*****
AF113214      1501 CAATTTGGAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTG
ss.DNA40370   1616 TTTTGATCAAATAAAGGATGATAATAGATATTA
*****
AF113214      1561 TTTTGATCAAATAAAGGATGATAATAGATATTA

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>30 P\_AAC75884 Human ORFX ORF1439 polynucleotide sequence SEQ ID NO:2877. (1921 bp) [1 seg]

Score = 1543 (3059 bits), Expect = 0.0

Identities = 1619/1642 (98%), Gaps = 3/1642 (0%), at 8,2-1649,1640, Strand +/+

ss.DNA40370	8	GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
		*****
P_AAC75884	2	GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
ss.DNA40370	68	GGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
		*****
P_AAC75884	62	GGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
ss.DNA40370	128	CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
		*****
P_AAC75884	122	CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
ss.DNA40370	188	TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
		*****
P_AAC75884	182	TCTGGTGGCTCTATTATGCCACCA-CTCCTGCAAGAACTTC--AGAAGTCCCCCTGGTCA
ss.DNA40370	248	TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
		*****
P_AAC75884	239	TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTG
ss.DNA40370	308	GGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCC
		*****
P_AAC75884	299	GGCCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCCAGTCTCC
ss.DNA40370	368	TATTTGTGGATAATCCCGTGGGCACTGGGTTAGTTATGTGAATGGTAGTGGTGCCTATG
		*****
P_AAC75884	359	TATTTGTGGATAATCCCGTGGGCACTGGGTTAGTTATGTGAATGGTAGTGGTGCCTATG
ss.DNA40370	428	CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
		*****
P_AAC75884	419	CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
ss.DNA40370	488	GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
		*****
P_AAC75884	479	GCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
ss.DNA40370	548	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
		*****
P_AAC75884	539	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
ss.DNA40370	608	ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT
		*****
P_AAC75884	599	ACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTGGTGCTCTCCT
ss.DNA40370	668	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
		*****
P_AAC75884	659	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
ss.DNA40370	728	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
		*****
P_AAC75884	719	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC



ss.DNA40370	788	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA *****
P_AAC75884	779	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
ss.DNA40370	848	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC *****
P_AAC75884	839	TCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
ss.DNA40370	908	ACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC *****
P_AAC75884	899	ACCTAGTTTGTCTCTGTCTAGCGCCACGTGAGACACCTACAACGAGACGCCTTAAGCCAGC
ss.DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG *****
P_AAC75884	959	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
ss.DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA *****
P_AAC75884	1019	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATCGACA
ss.DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC *****
P_AAC75884	1079	TTGTGGATACGTTGCTGGAGGCAGGGGTCAATGTGACTGTGTATAATGGGCAGCTGGATC
ss.DNA40370	1148	TCATCGTAGATACCATGGGTCTAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGC **** *
P_AAC75884	1139	TCATTGTGGACACCATAGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGTGT
ss.DNA40370	1208	CTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT * *
P_AAC75884	1199	CCAGATTCAATCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACAT
ss.DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA *****
P_AAC75884	1259	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
ss.DNA40370	1328	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG *****
P_AAC75884	1319	TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
ss.DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA *****
P_AAC75884	1379	AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
ss.DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG *****
P_AAC75884	1439	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
ss.DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT *****
P_AAC75884	1499	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
ss.DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA *****
P_AAC75884	1559	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTGATCAAAA
ss.DNA40370	1628	TAAAGGATGATAATAGATATTA *****

P\_AAC75884 1619 TAAAGGATGATAATAGATATTA

>31 P\_ABK30363 Human G-protein-coupled protease #133. cDNA, PAT 23-APR-2002  
(1960 bp) [1 seg]

Score = 1407 (2789 bits), Expect = 0.0

Identities = 1620/1658 (97%), Gaps = 26/1658 (1%), at 17,11-1649,1667, Strand  
+ / +

ss.DNA40370	17	GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGT-GGTTG
		***** ** **
P_ABK30363	11	GCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGAAGGATG
ss.DNA40370	76	CTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAG
		*****
P_ABK30363	71	CTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGCCACAGAG
ss.DNA40370	136	GAGGGCAAGG--AAGTAT-GGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG
		***** * ***
P_ABK30363	131	GAGGGCAAGGGAACCTTATGGGGATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGG
ss.DNA40370	193	TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGG
		*****
P_ABK30363	191	TGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCATGTGG
ss.DNA40370	253	CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGGAGAAATTGGGCCC
		*****
P_ABK30363	251	CTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGGAGAAATTGGGCCC
ss.DNA40370	313	CTTGACAGTGATCTCAAACAC-GGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATT
		*****
P_ABK30363	311	CTTGACAGTGATCTCAAACACGGGAAAACACCTGGCTCCAGGCTGCCAGTCTCCTATT
ss.DNA40370	372	TGTGGATAATCCCGT-GGGCACTGGGTTTCAGTTATGTGAATGGT-AGTGGTGCCTATGCC
		*****
P_ABK30363	371	TGTGGATAATCCCGTAGGGCACTGGGTTTCAGTTATGTGAATGGTAAGTGGTGCCTATGCC
ss.DNA40370	430	AAGGACCTGGC-TATGGTGGCTTCAGACAT-GATGGTTCTCCTGAAGACCTTCTTCAGTT
		*****
P_ABK30363	431	AAGGACCTGGCTTATGGTGGCTTCAGACATGGATGGTTCTCCTGAAGACCTTCTTCAGTT
ss.DNA40370	488	GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
		*****
P_ABK30363	491	GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
ss.DNA40370	548	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
		*****
P_ABK30363	551	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTAGCGAGGGACCATCAAGTGCA
ss.DNA40370	608	ACTTTGCGGGGGTTGCCTTGGGTGATTCTGATCTCCCCTGTTGATTGGTGCTCTCCT
		*****
P_ABK30363	611	ACTTTGCGGGGGTTGCCTTGGGTGATTCTGATCTCCCCTGTTGATTGGTGCTCTCCT
ss.DNA40370	668	GGGGACC-TTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCT
		*****
P_ABK30363	671	GGGGACCATTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCT
ss.DNA40370	727	AAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAG
		*****

P\_ABK30363 731 AAGGTTGCAGAGCAAGT-CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAG  
 ss.DNA40370 787 CTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTA-TAA  
 \*\*\*\*\*  
 P\_ABK30363 790 CTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATTAA  
 ss.DNA40370 846 CATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTC-TAGAATTCACACAGA  
 \*\*\*\*\*  
 P\_ABK30363 850 CATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCCTTAGAATTCACACAGA  
 ss.DNA40370 905 GCCACCTAGTTTGTCTTTGTCTCAGCGCCACGTG-AGACACCTACAACGAGATGCCTTAAGC  
 \*\*\*\*\*  
 P\_ABK30363 910 GCCACCTAGTTTGTCTTTGTCTCAGCGCCACGTGAAGACACCTTACACGAGATGCCTTAAGC  
 ss.DNA40370 964 CAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGG  
 \*\*\*\*\*  
 P\_ABK30363 970 CAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGG  
 ss.DNA40370 1024 GGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATT  
 \*\*\*\*\*  
 P\_ABK30363 1030 GGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATT  
 ss.DNA40370 1084 AGCATTGTGGA-CGAGTTGCTGGAGGCAGGGATCAA-CGTGA-CGGTGTA-TAATGGAC-  
 \*\*\*\*\* \* \*\*\*\*\*  
 P\_ABK30363 1090 AGCATTGTGGACCAAGTTGCTGGAGGCAGGGATCAACCGTGACCGGTGTATTAATGGACA  
 ss.DNA40370 1139 AGC-TGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGG  
 \*\*\* \*\*\*\*\*  
 P\_ABK30363 1150 AGCTTGGATCTCATCGTAGATACCATGGGTGAGGAGCCTGGGTGCGGAAACTGAAGTGG  
 ss.DNA40370 1198 CCAGAACTGCCTAAATTCAGTCAGCTGAAGT-GGAAGGCCCTGTACAGTGACCCTAAATC  
 \*\*\*\*\*  
 P\_ABK30363 1210 CCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGGAAGGCCCTGTACAGTGACCCTAAATC  
 ss.DNA40370 1257 TTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAA  
 \*\*\*\*\*  
 P\_ABK30363 1270 TTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAA  
 ss.DNA40370 1317 AGCTGGTCATATGGTTCCTTCTGACCAA-GGGGACATGGCTCTGAAGATGATGAGACTGG  
 \*\*\*\*\*  
 P\_ABK30363 1330 AGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG  
 ss.DNA40370 1376 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTT-TGGCCTTGGGGCAC  
 \*\*\*\*\*  
 P\_ABK30363 1390 TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTATGGCCTTGGGGCAC  
 ss.DNA40370 1435 AGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAAC-TG  
 \*\*\*\*\*  
 P\_ABK30363 1450 AGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTTG  
 ss.DNA40370 1494 GGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCA-TTGTCTCTGG  
 \*\*\*\*\*  
 P\_ABK30363 1510 GGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTTGTCTCTGG  
 ss.DNA40370 1553 AGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAA-TTGA  
 \*\*\*\*\*  
 P\_ABK30363 1570 AGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGA

ss.DNA40370 1612 TTTGTTTTGATCAAAATAAAGGATGATAATAGATATTA  
\*\* \*\*

P\_ABK30363 1630 TTCGTTTCGATCAAAATAAAGGATGATAATAGATATTA

>32 P\_AAH89926 Human bone marrow cDNA, SEQ ID NO: 57. cDNA, PAT 01-OCT-2001  
(1940 bp) [1 seg]  
Score = 1389 (2753 bits), Expect = 0.0  
Identities = 1577/1629 (96%), Gaps = 13/1629 (0%), at 34,10-1649,1638, Strand  
+ / +

ss.DNA40370 34 ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG  
\*\*\*\*\*

P\_AAH89926 10 ATGGAGCTGGCACTGCGGCGCTCTCCCGTTCGCTGTGGTTGCTGGAGCTGCCGCTGCTA

ss.DNA40370 94 CTGGGCCTGAACGCAGGAGCTGTCAATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGG  
\*\*\*\*\*

P\_AAH89926 70 CTGGGCCTGAACGCAAGAGCTGTCAATTGACTGCCCCACAGAGGAGGGCAAGGAACCATGG

ss.DNA40370 154 GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC  
\*\*\*\*\*

P\_AAH89926 130 GATTATGTGACGGTTCGCAAGGATGCCTACATGTTCTGGTGGGTATATTATGCCACCAAC

ss.DNA40370 214 TCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT  
\* \*\*\*\*\*

P\_AAH89926 190 TTCTGCAAGAACTTTTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTGCAGGCGGT

ss.DNA40370 274 TCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCTTGACAGTGATCTCAAACCA  
\*\*\*\*\*

P\_AAH89926 250 TCTAACACTGGATTTGGAACTCTGAGGAAATTGGGCCCTTGACAGTGATCTCAAACCA

ss.DNA40370 334 CGGAAAACCACTGG- - - -CTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGG  
\*\*\*\*\*

P\_AAH89926 310 CGGAAAACCACTGGGTACACTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGG

ss.DNA40370 389 GCACTGGGTTCACTTATGTGAATGGTAGTGGTGCC-TATGCCAAGGACCTGGCTATGGTG  
\*\*\*\*\*

P\_AAH89926 370 GCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCCTATGCCAAGGACCTGGCTATGGTG

ss.DNA40370 448 GCTTCAGACATGATGG-TTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC  
\*\*\*\*\*

P\_AAH89926 430 GCTTCAGACATGATGGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCCAGAC

ss.DNA40370 507 AGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGCATTTGGTCT  
\*\*\*\*\*

P\_AAH89926 490 AGTTCCATTGTACATTTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGCATTTGGTCT

ss.DNA40370 567 AGAGCTTTATAAGGCCATTTCAGCGAGGGACC-ATCAAGTGCAACTTTGCGGGGGTTGCCT  
\*\*\*\*\*

P\_AAH89926 550 AGAGCTTTATAAGGCCATTTCAGCGAGGGACCCATAAAGTGCAACTTTGCGGGGGTTGCCT

ss.DNA40370 626 TGGGTGATTCTCGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGTACA  
\*\*\*\*\*

P\_AAH89926 610 TGGGTGATTCTCGAATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGTACA

ss.DNA40370 686 GCATGTCTCTT-CTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
\*\*\*\*\*

P\_AAH89926 670 GCATGTCTCTTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA

ss.DNA40370	745	CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAA
P_AA89926	730	CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAA
ss.DNA40370	805	ATGATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACTAAAAGCACT
P_AA89926	790	ATGATCATTGAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACTAAAAGCACT
ss.DNA40370	865	CCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGT
P_AA89926	850	CCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGT
ss.DNA40370	925	CAGCGCCACGTGAGACACCTACAACGAGATGC-CTTAAGCC-AGCTCATGAATGGCCCCA
P_AA89926	910	CAGCGCCACGTGAGACACCTACAACGATATGCACCTAAGCCTATTTTCATGAACGGCCCCA
ss.DNA40370	983	TCAGAAAGAAGCTCAAAATTATTCTTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACG
P_AA89926	970	TCAAAAAGAAACCCAAAATTATTCTGACGATCCTTCCTGGGTAGGCCAGGCTACCAACG
ss.DNA40370	1043	TCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGC
P_AA89926	1030	TCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAACATTGTGGACGAGTTGC
ss.DNA40370	1103	TGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCA
P_AA89926	1090	TGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTACATACCA
ss.DNA40370	1163	TGGGTGAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGC
P_AA89926	1150	TGGGTGAGGAGGCCTGGGTGCGGAACTGAAGTGGCCAGAAGTGCCTAAATTCAGTCAGC
ss.DNA40370	1223	TGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGT
P_AA89926	1210	TGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGT
ss.DNA40370	1283	CCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACC
P_AA89926	1270	CCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACC
ss.DNA40370	1343	AAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGG
P_AA89926	1330	AAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGG
ss.DNA40370	1403	GCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGT
P_AA89926	1390	GCTGGAGATGAGCCGTTTGGCCTTGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGT
ss.DNA40370	1463	AGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGC
P_AA89926	1450	AGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAGAAGGTTCTGACCAGC
ss.DNA40370	1523	TTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTA
P_AA89926	1510	TTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAATTATTTCTGCTTCTTA
ss.DNA40370	1583	AAAAAA-CCTAAGA-TTTTTTAAAAAATTGATTTGTTTGGATCAAAATAAAGGATGATAA

P\_AAH89926 1570 AAAAAACCCTAAGATTTTTTTTAAAAATTGATTATTTTTTGATCAAACCAAAGGATGATAA  
 ss.DNA40370 1641 TAGATATTA  
 \*\*\*\*\*  
 P\_AAH89926 1630 TAGATATTA

>33 AX191553 Sequence 75 from Patent WO0149728. DNA, linear, PAT 15-AUG-2001  
 (1359 bp) [1 seg]  
 Score = 1355 (2686 bits), Expect = 0.0  
 Identities = 1358/1359 (99%), at 34,1-1392,1359, Strand +/+

ss.DNA40370 34 ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG  
 \*\*\*\*\*  
 AX191553 1 ATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTG  
 ss.DNA40370 94 CTGGGCCTGAACGCAGGAGCTGTCAATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGG  
 \*\*\*\*\*  
 AX191553 61 CTGGGCCTGAACGCAGGAGCTGTCAATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGG  
 ss.DNA40370 154 GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC  
 \*\*\*\*\*  
 AX191553 121 GATTATGTGACGGTCCGCAAGGATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAAC  
 ss.DNA40370 214 TCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT  
 \*\*\*\*\*  
 AX191553 181 TCCTGCAAGAACTTCTCAGAACTGCCCCTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGT  
 ss.DNA40370 274 TCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCA  
 \*\*\*\*\*  
 AX191553 241 TCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGCCCCTTGACAGTGATCTCAAACCA  
 ss.DNA40370 334 CGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACT  
 \*\*\*\*\*  
 AX191553 301 CGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACT  
 ss.DNA40370 394 GGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCA  
 \*\*\*\*\*  
 AX191553 361 GGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGACCTGGCTATGGTGGCTTCA  
 ss.DNA40370 454 GACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCAGACAGTTCCA  
 \*\*\*\*\*  
 AX191553 421 GACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAGAATTCAGACAGTTCCA  
 ss.DNA40370 514 TTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTT  
 \*\*\*\*\*  
 AX191553 481 TTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTT  
 ss.DNA40370 574 TATAAGGCCATTACAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGAT  
 \*\*\*\*\*  
 AX191553 541 TATAAGGCCATTACAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGAT  
 ss.DNA40370 634 TCCTGGATCTCCCCTGTTGATTGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCT  
 \*\*\*\*\*  
 AX191553 601 TCCTGGATCTCCCCTGTTGATTGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCT  
 ss.DNA40370 694 CTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCC  
 \*\*\*\*\*  
 AX191553 661 CTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCC

ss.DNA40370	754	GTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATT
		*****
AX191553	721	GTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATT
ss.DNA40370	814	GAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAGCACTCCACGTCT
		*****
AX191553	781	GAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAGCACTCCACGTCT
ss.DNA40370	874	ACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCAC
		*****
AX191553	841	ACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCAC
ss.DNA40370	934	GTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAG
		*****
AX191553	901	GTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAAG
ss.DNA40370	994	CTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAAC
		*****
AX191553	961	CTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAAC
ss.DNA40370	1054	ATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGG
		*****
AX191553	1021	ATGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGG
ss.DNA40370	1114	ATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCTAGGAG
		*****
AX191553	1081	ATCAACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCTAGGAG
ss.DNA40370	1174	GCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAG
		*****
AX191553	1141	GCCTGGGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAG
ss.DNA40370	1234	GCCCTGTACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAAC
		*****
AX191553	1201	GCCCTGTACAGTGACCCTAAATCTCTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAAC
ss.DNA40370	1294	CTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATG
		*****
AX191553	1261	CTTGCTTTCTACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATG
ss.DNA40370	1354	GCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG
		*****
AX191553	1321	GCTCTGAAGATGATGAGACTGGTGACTCAGCAAGAATAG

GenBank (Release 134, feb 2003)

P\_AAF30502 Human PRO302 cDNA clone DNA40370-1217. 650 bp,  
cDNA, PAT 29-MAY-2001

ACCESSION P\_AAF30502

KEYWORDS PRO302; vitellogenic carboxypeptidase homologue; human;  
angiogenesis; cardiovascularisation; trauma; wound; cancer;  
atherosclerosis; cardiac hypertrophy; macular degeneration;  
cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
antirheumatic; antiarthritic; antiinflammatory; vulnerary;  
antitumour; diagnosis; gene therapy; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Fong,S., Gerritsen,M.E., Goddard,A., Gurney,A.L., Hillan,K.J.  
Williams,P.M., Wood,W.I.

TITLE Composition comprising a PRO230, PRO216 or PRO302 polypeptide,  
agonist or antagonist for promoting or inhibiting angiogenesis  
and/or cardiovascularisation in mammals -

JOURNAL Patent: WO200119987-A1; Filing Date: 29-NOV-1999; 99WO-US28214;  
Publication Date: 22-MAR-2001; Priority: 13-SEP-1999;  
99WO-US20944. 15-SEP-1999; 99WO-US21090; Assignee: (GETH )  
GENENTECH INC; Cross Reference: WPI; 2001-235264/24. P-PSDB;  
AAB20341; Patent Format: Claim 56; Fig 5; 141pp; English.

COMMENT The present sequence is that of cDNA clone DNA40370-1217 (ATCC  
209485) encoding human PRO302 (see AAB20341), a vitellogenic  
carboxypeptidase homologue. The cDNA was isolated following  
expressed sequence tag database searches using extracellular domains  
of about 950 known secreted sequences, use of isolated sequences to  
design PCR primers and probe (see AAF30509-12), screening of cDNA  
libraries, and isolation from a foetal lung tissue library. PRO302  
is 1 of 3 novel PRO proteins of the invention. PRO230, PRO216 and  
PRO302 polynucleotides and polypeptides, recombinant retroviral  
particles, ex vivo producer cells, expression vectors, host cells,  
and methods of recombinant production are provided, as well as  
antibodies, agonists and antagonists. The polynucleotides,  
polypeptides, agonists and antagonists are useful for treating or  
diagnosing a cardiovascular, endothelial or angiogenic disorder in a  
mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related  
macular degeneration (all claimed), atherosclerosis, hypertension,  
arterial restenosis, rheumatoid arthritis, angina, myocardial  
infarction, thrombophlebitis and lymphangitis. The polypeptides,  
agonists and antagonists are also used in claimed methods of  
stimulating or inhibiting endothelial cell growth.

FEATURES Location/Qualifiers

CDS 34..1392

/\*tag= a

sig\_peptide 34..108

/\*tag= b

mat\_peptide 109..1389

/\*tag= c

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

P\_AAA13199 PRO302, vitellogenic carboxypeptidase homologue nucleotide sequence.  
650 bp, cDNA, PAT 20-JUL-2000

ACCESSION P\_AAA13199

KEYWORDS Human; PRO302; Vitellogenic carboxypeptidase; cardiant; angiogenic;



cytostatic; ophthalmic; antiproliferative activity; ss;  
cardiovascular; endothelial; angiogenic disorder; cardiac  
hypertrophy; trauma; cancer; myocardial infarction; age-related  
macular degeneration; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Fong,S., Gerritsen,M.E., Goddard,A., Gurney,A.L., Hillan,K.J.  
Williams,P.M., Wood,W.I.

TITLE A composition comprising PRO230, PRO216 or PRO302 polypeptides,  
agonists or antagonists useful for promotion or inhibition of  
cardiovascularisation, angiogenesis or endothelialisation in mammals

JOURNAL Patent: WO200015792-A2; Filing Date: 13-SEP-1999; 99WO-US20944;  
Publication Date: 23-MAR-2000; Priority: 14-SEP-1998;  
98US-0100262. 14-SEP-1998; 98WO-US19177; Assignee: (GETH )  
GENENTECH INC; Cross Reference: WPI; 2000-271431/23; Patent Format:  
Example 3; Fig 5; 135pp; English.

COMMENT This sequence represents the nucleotide sequence encoding a human  
PRO302 protein. PRO302 is a human vitellogenic carboxypeptidase  
homologue. The invention relates to a composition comprising a  
PRO230 (tubulointerstitial nephritis antigen homologue), PRO216  
(osteomodulin/fibromodulin homologue) or PRO302 (vitellogenic  
carboxypeptidase homologue) polypeptide, or an agonist or antagonist  
of these. Also included in the invention is a method for preparing  
the composition, agonists and antagonists of PRO230, PRO216 or  
PRO302, and antibodies that bind to a PRO230, PRO216 or PRO302  
polypeptides. The composition of the invention has cardiant,  
angiogenic, cytostatic, ophthalmic, and antiproliferative activity.  
Analysis of the level of expression of a gene encoding a PRO230,  
PRO216 or PRO302 polypeptide or detecting the presence/absence of  
the polypeptide is useful for diagnosis of cardiovascular,  
endothelial or angiogenic disorders in mammals. Anti-PRO230, PRO216  
or PRO302 antibodies are useful in these diagnostic methods. The  
PRO230, PRO216 or PRO302 polypeptides (and their coding sequences),  
agonists and antagonists are useful for treatment of cardiovascular,  
endothelial or angiogenic disorders, especially cardiac hypertrophy  
(especially characterized by presence of an elevated level of  
PGF-2alpha), trauma or cancer, myocardial infarction or age-related  
macular degeneration. In particular, PRO216, an agonist of PRO216,  
an antagonist of PRO230, PRO216 or PR302 or an anti-PRO216 antibody  
is useful for inhibition of endothelial cell growth in a mammal.  
Endothelial cell growth can be stimulated by administration of  
PRO230, a PRO230 agonist or antagonist or an anti-PRO230 antibody.  
Additionally, an anti-PRO302 antibody can inhibit angiogenesis  
induced by PRO302 in a mammal.

FEATURES Location/Qualifiers

CDS

34..1392

/\*tag= a

/product= PRO302

/note= "Vitellogenic carboxypeptidase homologue"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

P\_AAX52258 Protein PRO302 cDNA clone DNA40370-1217. 650 bp,  
DNA, PAT 25-JUN-1999

ACCESSION P\_AAX52258

KEYWORDS Secreted protein; transmembrane protein; human; enterocolitis;

Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Chen, J., Goddard, A., Gurney, A.L., Pennica, D., Wood, W.I., Yuan, J.

TITLE New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration

JOURNAL Patent: WO9914328-A2; Filing Date: 16-SEP-1998; 98WO-US19330; Publication Date: 25-MAR-1999; Priority: 25-NOV-1997;

97US-0066840. 17-SEP-1997; 97US-0059113. 17-SEP-1997;

97US-0059115. 17-SEP-1997; 97US-0059117. 17-SEP-1997;

97US-0059119. 17-SEP-1997; 97US-0059121. 17-SEP-1997;

97US-0059122. 17-SEP-1997; 97US-0059184. 18-SEP-1997;

97US-0059263. 18-SEP-1997; 97US-0059266. 15-OCT-1997;

97US-0062125. 17-OCT-1997; 97US-0062285. 17-OCT-1997;

97US-0062287. 21-OCT-1997; 97US-0063486. 24-OCT-1997;

97US-0062814. 24-OCT-1997; 97US-0062816. 24-OCT-1997;

97US-0063045. 24-OCT-1997; 97US-0063120. 24-OCT-1997;

97US-0063121. 24-OCT-1997; 97US-0063127. 24-OCT-1997;

97US-0063128. 27-OCT-1997; 97US-0063329. 27-OCT-1997;

97US-0063327. 28-OCT-1997; 97US-0063541. 28-OCT-1997;

97US-0063542. 28-OCT-1997; 97US-0063544. 28-OCT-1997;

97US-0063549. 28-OCT-1997; 97US-0063550. 28-OCT-1997;

97US-0063564. 29-OCT-1997; 97US-0063435. 29-OCT-1997;

97US-0063704. 29-OCT-1997; 97US-0063732. 29-OCT-1997;

97US-0063738. 29-OCT-1997; 97US-0063734. 29-OCT-1997;

97US-0064215. 29-OCT-1997; 97US-0063735. 31-OCT-1997;

97US-0063870. 31-OCT-1997; 97US-0064103. 03-NOV-1997;

97US-0064248. 07-NOV-1997; 97US-0064809. 12-NOV-1997;

97US-0065186. 17-NOV-1997; 97US-0065846. 18-NOV-1997;

97US-0065693. 21-NOV-1997; 97US-0066120. 21-NOV-1997;

97US-0066364. 24-NOV-1997; 97US-0066772. 24-NOV-1997;

97US-0066466. 24-NOV-1997; 97US-0066770. 24-NOV-1997;

97US-0066511. 24-NOV-1997; 97US-0066453; Assignee: (GETH )

GENENTECH INC; Cross Reference: WPI; 1999-229533/19. P-PSDB;

AAY13387; Patent Format: Claim 2; Fig 89; 320pp; English.

COMMENT AAX52213-74 encode secreted and transmembrane human proteins, and are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g.

for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

FEATURES                      Location/Qualifiers  
 BASE COUNT            414 a      365 c      453 g      418 t  
 ORIGIN

P\_AAX25445 Human PRO216 cDNA clone UNQ265. 650 bp, cDNA, PAT 19-JUL-1999

ACCESSION P\_AAX25445

KEYWORDS PRO302; vitellogenic carboxypeptidase; human; angiogenesis; cardiovascularisation; wound healing; cancer; atherosclerosis; cardiac hypertrophy; myocardial infarction; antiangiogenic; antitumour; tissue regeneration; pulmonary fibrosis; neurological disease; macular degeneration; diagnosis; therapy; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Fong,S., Gerritsen,M.E., Goddard,A., Gurney,A.L., Hillan,K. Williams,P.M., ,W. Odwi;

TITLE Composition containing human polypeptides with anti-angiogenic activity

JOURNAL Patent: WO9914234-A2; Filing Date: 14-SEP-1998; 98WO-US19177; Publication Date: 25-MAR-1999; Priority: 24-NOV-1997; 97US-0066772. 17-SEP-1997; 97US-0059117. 27-OCT-1997; 97US-0063329; Assignee: (GETH ) GENENTECH INC; Cross Reference: WPI; 1999-254381/21. P-PSDB; AAY05768; Patent Format: Example 1; Fig 8; 102pp; English.

COMMENT This is the DNA sequence of human cDNA clone UNQ265 or DNA40370-1217 (ATCC 209485), which encodes PRO302, identified as a vitellogenic carboxypeptidase homologue (see AAY05768). The cDNA clone was isolated from a human foetal kidney tissue cDNA library using a probe and primers (see AAX25456-59) based on a consensus sequence (see AAX25449) for PRO302 that had been deduced from a set of overlapping EST clones (see AAX25446-48). Compositions containing PRO302, PRO216 (human osteomodulin, see AAY05767) and PRO230 in admixture with a carrier are claimed. The compositions are used to treat or prevent a wide range of cardiovascular, endothelial and angiogenic disorders (claimed), specifically cardiac hypertrophy (especially where associated with elevated levels of prostaglandin F2 alpha or induced by myocardial infarction), trauma (wounds, burns, or tissue regeneration more generally, including neurological disease), and cancer. Antagonists may be used similarly, also to treat age-related macular degeneration (or other angiogenic retinal disorders) and to prevent excessive growth of connective tissue during wound healing or in pulmonary fibrosis.

FEATURES                      Location/Qualifiers  
 CDS                            34..1392  
                               /\*tag= a  
 sig\_peptide                34..108  
                               /\*tag= b  
 mat\_peptide                109..1289  
                               /\*tag= c

BASE COUNT        414 a        365 c        453 g        418 t  
ORIGIN

— P\_AAF72416 Human PRO302 cDNA. 650 bp, cDNA, PAT 24-APR-2001

ACCESSION    P\_AAF72416

KEYWORDS     Human; PRO; dermatological; antipsoriatic; cytostatic;  
antiinflammatory; antiparkinsonian nootropic; neuroprotective;  
vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic;  
antirheumatic; cancer; antiarthritic; antiinfertility; antidiabetic;  
antiviral; diabetes; ophthalmological; gene therapy; skin disease;  
gastrointestinal disorder; ischaemia; inflammation; patent; GENESEQ  
patentdb.

SOURCE       Homo sapiens.

ORGANISM      Homo sapiens.

REFERENCE     1 (bases 1 to 1650)

0    AUTHORS    Ashkenazi,A.J., Botstein,D., Desnoyers,L., Eaton,D.L.,  
Ferrara,N. Filvaroff,E., Fong,S., Gao,W., Gerber,H.,  
Gerritsen,M.E., Goddard,A. Godowski,P.J., Grimaldi,C.J.,  
Gurney,A.L., Hillan,K.J., Kljavin,I.J. Mather,J.P., Pan,J.,  
Paoni,N.F., Roy,M.A., Stewart,T.A., Tumas,D. Williams,P.M.,  
Wood,W.I.

TITLE         Sixty one nucleic acids encoding PRO polypeptides which are useful  
in the treatment of skin diseases (e.g. psoriasis), cancers (e.g.  
lung squamous cell carcinoma) and neurodegenerative diseases (e.g.  
Alzheimer's disease) -

JOURNAL       Patent: WO200104311-A1; Filing Date: 22-FEB-2000; 2000WO-US04414;  
Publication Date: 18-JAN-2001; Priority: 07-JUL-1999;  
99US-0143048. 26-JUL-1999;    99US-0145698. 28-JUL-1999;  
99US-0146222. 08-SEP-1999;    99WO-US20594. 13-SEP-1999;  
99WO-US20944. 15-SEP-1999;    99WO-US21090. 15-SEP-1999;  
99WO-US21547. 05-OCT-1999;    99WO-US23089. 29-NOV-1999;  
99WO-US28214. 30-NOV-1999;    99WO-US28313. 16-DEC-1999;  
99WO-US30095. 20-DEC-1999;    99WO-US30911. 20-DEC-1999;  
99WO-US30999. 05-JAN-2000;    99WO-US00219; Assignee: (GETH )  
GENENTECH INC; Cross Reference: WPI; 2001-081051/09. P-PSDB;  
AAB80255; Patent Format: Claim 2; Fig 89; 393pp; English.

COMMENT       The present sequence is one of sixty one nucleic acids encoding  
novel secreted and transmembrane PRO polypeptides. The PRO  
polypeptides are useful for treating skin diseases (e.g. psoriasis),  
cancers (e.g. lung squamous cell carcinoma), gastrointestinal  
disorders (e.g. enterocolitis), neurodegenerative diseases (e.g.  
Alzheimer's disease, Parkinson's disease), wound repair,  
cardiovascular disorders (e.g. endometrial bleeding angiogenesis,  
ischaemias such as coronary ischaemia, atherosclerosis),  
inflammatory disorders (e.g. asthma, rheumatoid arthritis, multiple  
sclerosis), infertility, AIDS and diabetes and retinal disorders  
such as retinitis pigmentosum. The PRO nucleic acids have  
applications in molecular biology, including use as hybridization  
probes, and in chromosome and gene mapping.

FEATURES                    Location/Qualifiers

BASE COUNT        414 a        365 c        453 g        418 t  
ORIGIN

— P\_ABL95586 Human angiogenesis related cDNA PRO302 SEQ ID NO: 51. 650 bp,  
cDNA, PAT 19-JUL-2002

ACCESSION    P\_ABL95586

KEYWORDS     Human; angiogenesis; PRO protein; cardiovascularisation; wound;  
cancer; atherosclerosis; cardiac hypertrophy; gene therapy;

endothelial disorder; cardiant; cytostatic; antiangiogenic;  
hypotensive; vulnerary; antiarteriosclerotic; gene; patent; GENESEQ  
patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.F., Watanabe, C.K., Williams, P.M., Wood, W.I.,  
Ye, W.

TITLE One hundred and eighty seven nucleic acids encoding PRO  
polypeptides, useful in diagnosis and treatment of cardiovascular  
(e.g. myocardial infarction), endothelial or angiogenic disorders in  
a mammal -

JOURNAL Patent: WO200208284-A2; Filing Date: 09-JUL-2001; 2001WO-US21735;  
Publication Date: 31-JAN-2002; Priority: 20-JUL-2000;  
2000US-219556P. 25-JUL-2000; 2000US-220624P. 25-JUL-2000;  
2000US-220664P. 28-JUL-2000; 2000WO-US20710. 02-AUG-2000;  
2000US-222695P. 17-AUG-2000; 2000US-0643657. 23-AUG-2000;  
2000WO-US23522. 24-AUG-2000; 2000WO-US23328. 07-SEP-2000;  
2000US-230978P. 15-SEP-2000; 2000US-000000P. 18-SEP-2000;  
2000US-0664610. 18-SEP-2000; 2000US-0665350. 24-OCT-2000;  
2000US-242922P. 08-NOV-2000; 2000US-0709238. 08-NOV-2000;  
2000WO-US30952. 10-NOV-2000; 2000WO-US30873. 01-DEC-2000;  
2000WO-US32678. 20-DEC-2000; 2000US-0747259. 20-DEC-2000;  
2000WO-US34956. 22-JAN-2001; 2001US-0767609. 28-FEB-2001;  
2001US-0796498. 28-FEB-2001; 2001WO-US06520. 01-MAR-2001;  
2001WO-US06666. 09-MAR-2001; 2001US-0802706. 14-MAR-2001;  
2001US-0808689. 22-MAR-2001; 2001US-0816744. 05-APR-2001;  
2001US-0828366. 10-MAY-2001; 2001US-0854208. 10-MAY-2001;  
2001US-0854280. 25-MAY-2001; 2001US-0866028. 25-MAY-2001;  
2001US-0866034. 25-MAY-2001; 2001WO-US17092. 30-MAY-2001;  
2001US-0870574. 30-MAY-2001; 2001WO-US17443. 01-JUN-2001;  
2001WO-US17800. 20-JUN-2001; 2001WO-US19692. 28-JUN-2001;  
2001WO-US00000; Assignee: (GETH ) GENENTECH INC. (BAKE/) BAKER K P.  
(FERR/) FERRARA N. (GERB/) GERBER H. (GERR/) GERRITSEN M E. (GODD/) GODDARD A. (GODO/) GODOWSKI P J. (GURN/) GURNEY A L. (HILL/) HILLAN K J. (MARS/) MARSTERS S A. (PANJ/) PAN J. (PAON/) PAONI N F. (STEP/) STEPHAN J F. (WATA/) WATANABE C K. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I; Cross Reference: WPI; 2002-171999/22. P-PSDB; ABB95448;  
Patent Format: Claim 1; Fig 51; 567pp; English.

COMMENT The present invention provides the protein and coding sequences of  
human PRO proteins. These are useful for treating or diagnosing a  
cardiovascular, endothelial or angiogenic disorder, including  
cardiac hypertrophy, trauma, cancer, age-related macular  
degeneration, atherosclerosis, hypertension, arterial restenosis,  
rheumatoid arthritis, angina, myocardial infarctions,  
thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast  
carcinoma and liver carcinoma) and wound healing. The present  
sequence is a coding sequence of the invention.

FEATURES Location/Qualifiers

BASE COUNT 414 a 365 c 453 g 418 t  
ORIGIN

P\_ABL88097 Human PRO302 cDNA sequence SEQ ID NO:51. 650 bp,  
cDNA, PAT 16-MAY-2002

ACCESSION P\_ABL88097

KEYWORDS Human; angiogenesis; cardiant; cytostatic; antiangiogenic;

hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A. Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.F., Watanabe, C.K., Williams, P.M., Wood, W.I., Ye, W.

TITLE One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

JOURNAL Patent: WO200200690-A2; Filing Date: 20-JUN-2001; 2001WO-US19692; Publication Date: 03-JAN-2002; Priority: 23-JUN-2000; 2000US-213637P. 20-JUL-2000; 2000US-219556P. 25-JUL-2000; 2000US-220624P. 25-JUL-2000; 2000US-220664P. 28-JUL-2000; 2000WO-US20710. 02-AUG-2000; 2000US-222695P. 17-AUG-2000; 2000US-0643657. 23-AUG-2000; 2000WO-US23522. 24-AUG-2000; 2000WO-US23328. 07-SEP-2000; 2000US-230978P. 18-SEP-2000; 2000US-0664610. 18-SEP-2000; 2000US-0665350. 24-OCT-2000; 2000US-242922P. 08-NOV-2000; 2000US-0709238. 08-NOV-2000; 2000WO-US30952. 10-NOV-2000; 2000WO-US30873. 01-DEC-2000; 2000WO-US32678. 20-DEC-2000; 2000US-0747259. 20-DEC-2000; 2000WO-US34956. 22-JAN-2001; 2001US-0767609. 28-FEB-2001; 2001US-0796498. 28-FEB-2001; 2001WO-US06520. 01-MAR-2001; 2001WO-US06666. 09-MAR-2001; 2001US-0802706. 14-MAR-2001; 2001US-0808689. 22-MAR-2001; 2001US-0816744. 05-APR-2001; 2001US-0828366. 10-MAY-2001; 2001US-0854208. 10-MAY-2001; 2001US-0854280. 25-MAY-2001; 2001US-0866028. 25-MAY-2001; 2001US-0866034. 25-MAY-2001; 2001WO-US17092. 30-MAY-2001; 2001US-0870574. 30-MAY-2001; 2001WO-US17443. 01-JUN-2001; 2001WO-US17800; Assignee: (GETH ) GENENTECH INC; Cross Reference: WPI; 2002-090516/12. P-PSDB; ABB84842; Patent Format: Claim 2; Fig 51; 565pp; English.

COMMENT ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.

FEATURES Location/Qualifiers

BASE COUNT 414 a 365 c 453 g 418 t

# ORIGIN

AX098272 Sequence 11 from Patent WO0119987. 1650 bp,  
DNA, linear, PAT 02-APR-2001

ACCESSION AX098272

VERSION AX098272.1 GI:13537577

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Fong, S., Gerritsen, M.E., Goddard, A., Gurney, A.L., Hillan, K.J.,  
Williams, P.M. and Wood, W.I.

TITLE Promotion or inhibition of angiogenesis and cardiovascularization

JOURNAL Patent: WO 0119987-A 11 22-MAR-2001;

Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..1650

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

AX454466 Sequence 51 from Patent WO0208284. 1650 bp,  
DNA, linear, PAT 06-JUL-2002

ACCESSION AX454466

VERSION AX454466.1 GI:21713857

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

JOURNAL Patent: WO 0208284-A 51 31-JAN-2002;

Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)

FEATURES Location/Qualifiers

source 1..1650

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

BD075577 Secretory and transmembrane polypeptide and nucleic acid encoding  
the same. 1650 bp, DNA, linear, PAT 27-AUG-2002

ACCESSION BD075577

VERSION BD075577.1 GI:22621180  
 KEYWORDS JP 2001516580-A/210.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1650)  
 AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Penica,D., Chen,J. and Yuan,J.  
 TITLE Secretory and transmembrane polypeptide and nucleic acid encoding  
 the same  
 JOURNAL Patent: JP 2001516580-A 210 02-OCT-2001;  
 GENENTECH INC  
 COMMENT OS Homo sapiens (human)  
 PN JP 2001516580-A/210  
 PD 02-OCT-2001  
 PF 16-SEP-1998 JP 2000511867  
 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR  
 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR  
 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR  
 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR  
 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR  
 17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR  
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 24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR  
 24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR  
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 28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR  
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 29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR  
 29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR  
 29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR  
 29-OCT-1997 US 60/064103,31-OCT-1997 US 60/063870 PR  
 03-NOV-1997 US 60/064248,07-NOV-1997 US 60/064809 PR  
 12-NOV-1997 US 60/065186,17-NOV-1997 US 60/065846 PR  
 18-NOV-1997 US 60/065693,21-NOV-1997 US 60/066120 PR  
 21-NOV-1997 US 60/066364,24-NOV-1997 US 60/066772 PR  
 24-NOV-1997 US 60/066466,24-NOV-1997 US 60/066770 PR  
 24-NOV-1997 US 60/066511,24-NOV-1997 US 60/066453 PR  
 25-NOV-1997 US 60/066840  
 PI WILLIAM I WOOD,AUSTIN L GURNEY,AUDLEY GODDARD,DIANE PENICA, PI  
 JEAN CHEN,  
 PI JEAN YUAN  
 PC C12N15/09,C07K14/47,C07K14/705,C07K16/18,C07K16/28,C07K19/00,  
 PC C12N1/19,  
 PC C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/02//(C12P21/08, PC  
 C12R1:91),  
 PC C12N15/00,C12N5/00  
 CC Secretory and transmembrane polypeptide and nucleic acid CC  
 encoding the same  
 FH Key Location/Qualifiers  
 FT source 1..1650  
 FT /organism='Homo sapiens (human)'.  
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 source 1..1650  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"



BASE COUNT	414 a	365 c	453 g	418 t
ORIGIN				

BD173394      Secreted and transmembrane polypeptides and nucleic acids encoding  
the same. 1650 bp, DNA, linear, PAT 18-FEB-2003

ACCESSION BD173394

VERSION BD173394.1 GI:28414705

KEYWORDS JP 2002238588-A/210.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding  
             the same

JOURNAL Patent: JP 2002238588-A 210 27-AUG-2002;  
GENENTECH INC

COMMENT	OS	Homo sapiens (human)
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PN JP 2002238588-A/210

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385315

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

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21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

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27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR

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31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR

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17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI  
JIAN ZHENG.

PI JEAN YUAN

PC C12N15/09, C07K14/435, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,

PC C12P21/02//C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19).

PC (C12N5/10, C12R1:91), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC

Secreted and transmembrane polypeptides and nucleic acids encoding the same

FH	Key	Location/Qualifiers
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FT source 1..1650  
 FT /organism='Homo sapiens (human)'.  
 FEATURES Location/Qualifiers  
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 BASE COUNT 414 a 365 c 453 g 418 t  
 ORIGIN

BD173075 Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same. 1650 bp, DNA, linear, PAT 18-FEB-2003

ACCESSION BD173075  
 VERSION BD173075.1 GI:28414384  
 KEYWORDS JP 2002238587-A/210.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and  
 Yuan,J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same

JOURNAL Patent: JP 2002238587-A 210 27-AUG-2002;  
 GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002238587-A/210

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385248

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

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17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR

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28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR

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31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR

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24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC

C12N15/02,  
PC  
C12P21/02,C12P21/08//(C12P21/02,C12R1:91),(C12P21/02,C12R1:19), PC  
(C12P21/02,C12R1:645),C12N15/00,C12N5/00,C12N15/00 CC Secreted  
and transmembrane polypeptides and nucleic CC acids encoding the  
same

FH Key Location/Qualifiers  
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FT /organism='Homo sapiens (human)'.  
FEATURES Location/Qualifiers

source 1..1650  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 414 a 365 c 453 g 418 t  
ORIGIN

AX490944 Sequence 51 from Patent WO0200690. 1650 bp,  
DNA, linear, PAT 16-AUG-2002

ACCESSION AX490944

VERSION AX490944.1 GI:22323809

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.

TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 51 03-JAN-2002;  
Genentech, Inc. (US)

FEATURES Location/Qualifiers  
source 1..1650  
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BASE COUNT 414 a 365 c 453 g 418 t  
ORIGIN

BD172756 Secreted and transmembrane polypeptides and nucleic acids encoding  
the same. 1650 bp, DNA, linear, PAT 18-FEB-2003

ACCESSION BD172756

VERSION BD172756.1 GI:28414060

KEYWORDS JP 2002238586-A/210.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and  
Yuan,J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same

JOURNAL Patent: JP 2002238586-A 210 27-AUG-2002;  
GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002238586-A/210  
 PD 27-AUG-2002  
 PF 18-DEC-2001 JP 2001385205  
 PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR  
 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR  
 17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR  
 17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR  
 18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR  
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 31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR  
 07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR  
 17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR  
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 24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR  
 24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI  
 WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI  
 JIAN ZHENG,  
 PI JEAN YUAN  
 PC C12N15/09,C07K14/47,C07K16/18,C07K19/00,C12N1/19,C12N1/21, PC  
 C12N5/10,  
 PC C12P21/02//C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),  
 PC  
 (C12N5/10,C12R1:91),(C12P21/02,C12R1:91),(C12P21/02,C12R1:645), PC  
 (C12P21/02,C12R1:19),(C12P21/08,C12R1:91),C12N15/00,C12N5/00, PC  
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 encoding the same  
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 BASE COUNT 414 a 365 c 453 g 418 t  
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 BD172437 Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same. 1650 bp, DNA, linear, PAT 18-FEB-2003  
 ACCESSION BD172437  
 VERSION BD172437.1 GI:28413737  
 KEYWORDS JP 2002223786-A/210.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and Yuan, J.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: JP 2002223786-A 210 13-AUG-2002; GENENTECH INC

COMMENT OS Homo sapiens (human)

PN JP 2002223786-A/210

PD 13-AUG-2002

PF 18-DEC-2001 JP 2001385135

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059117 PR

17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059121 PR

17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062125 PR

17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486, 24-OCT-1997 US 60/062816 PR

24-OCT-1997 US 60/062814, 24-OCT-1997 US 60/063127 PR

24-OCT-1997 US 60/063120, 24-OCT-1997 US 60/063121 PR

24-OCT-1997 US 60/063045, 24-OCT-1997 US 60/063128 PR

27-OCT-1997 US 60/063329, 27-OCT-1997 US 60/063327 PR

28-OCT-1997 US 60/063549, 28-OCT-1997 US 60/063541 PR

28-OCT-1997 US 60/063550, 28-OCT-1997 US 60/063542 PR

28-OCT-1997 US 60/063544, 28-OCT-1997 US 60/063564 PR

29-OCT-1997 US 60/063734, 29-OCT-1997 US 60/063738 PR

29-OCT-1997 US 60/063704, 29-OCT-1997 US 60/063435 PR

29-OCT-1997 US 60/064215, 29-OCT-1997 US 60/063735 PR

29-OCT-1997 US 60/063732, 31-OCT-1997 US 60/064103 PR

31-OCT-1997 US 60/063870, 03-NOV-1997 US 60/064248 PR

07-NOV-1997 US 60/064809, 12-NOV-1997 US 60/065186 PR

17-NOV-1997 US 60/065846, 18-NOV-1997 US 60/065693 PR

21-NOV-1997 US 60/066120, 21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772, 24-NOV-1997 US 60/066466 PR

24-NOV-1997 US 60/066770, 24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI

WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC C12N5/10,

PC

C12P21/02//C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC (C12P21/02, C12R1:645), C12N15/00, C12N5/00

CC Secreted and transmembrane polypeptides and nucleic CC acids encoding the same

FH Key Location/Qualifiers

FT source 1..1650

FT /organism='Homo sapiens (human)'. .

FEATURES Location/Qualifiers

source 1..1650

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 414 a 365 c 453 g 418 t

ORIGIN

BD175428 Secretory and transmembrane polypeptide and nucleic acid encoding

the same. 1650 bp, DNA, linear, PAT 18-MAR-2003

ACCESSION BDI75428

VERSION BDI75428.1 GI:29121126

KEYWORDS JP 2002253280-A/210.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1650)

AUTHORS Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and  
Yuan,J.

TITLE Secretory and transmembrane polypeptide and nucleic acid encoding  
the same

JOURNAL Patent: JP 2002253280-A 210 10-SEP-2002;  
GENENTECH INC

COMMENT OS Homo sapiens (human)  
PN JP 2002253280-A/210  
PD 10-SEP-2002  
PF 18-DEC-2001 JP 2001385319  
PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR  
17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR  
17-SEP-1997 US 60/059113,17-SEP-1997 US 60/059121 PR  
17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR  
18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR  
17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR  
21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR  
24-OCT-1997 US 60/062814,24-OCT-1997 US 60/063127 PR  
24-OCT-1997 US 60/063120,24-OCT-1997 US 60/063121 PR  
24-OCT-1997 US 60/063045,24-OCT-1997 US 60/063128 PR  
27-OCT-1997 US 60/063329,27-OCT-1997 US 60/063327 PR  
28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR  
28-OCT-1997 US 60/063550,28-OCT-1997 US 60/063542 PR  
28-OCT-1997 US 60/063544,28-OCT-1997 US 60/063564 PR  
29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR  
29-OCT-1997 US 60/063704,29-OCT-1997 US 60/063435 PR  
29-OCT-1997 US 60/064215,29-OCT-1997 US 60/063735 PR  
29-OCT-1997 US 60/063732,31-OCT-1997 US 60/064103 PR  
31-OCT-1997 US 60/063870,03-NOV-1997 US 60/064248 PR  
07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR  
17-NOV-1997 US 60/065846,18-NOV-1997 US 60/065693 PR  
21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR  
24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR  
24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR  
24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI  
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI  
JIAN ZHENG,  
PI JEAN YUAN  
PC C12N15/09,A61K45/00,A61P1/00,A61P13/12,A61P17/00,A61P17/06, PC  
A61P25/00,  
PC A61P25/16,A61P25/28,A61P31/12,A61P35/00,C07K14/47,C07K16/18,  
PC C07K19/00,  
PC C12N1/19,C12N1/21,C12N5/10//A61K38/00,A61K39/395,A61K39/395,  
PC A61P43/00,  
PC C12P21/08,(C12N1/19,C12R1:645),(C12N1/21,C12R1:19),(C12N5/10,  
PC C12R1:91),  
PC C12N15/00,C12N5/00,A61K37/02,(C12N5/00,C12R1:91) CC  
Secretory and transmembrane polypeptide and nucleic acid CC  
encoding the same

FH Key Location/Qualifiers  
 FT source 1..1650  
 FT /organism='Homo sapiens (human)'.  
 FEATURES Location/Qualifiers  
 source 1..1650  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 414 a 365 c 453 g 418 t  
 ORIGIN

P ABV72656 Human retinoid inducible serine carboxypeptidase cDNA. 921 bp,  
 cDNA, PAT 29-NOV-2002

ACCESSION P\_ABV72656

KEYWORDS Serine carboxypeptidase; mammalian; RISC; antihypertensive;  
 retinoid-inducible serine carboxypeptidase; antiarteriosclerotic;  
 nephrotropic; antiasthmatic; vasotropic; gene therapy; vascular  
 disease; vascular hyperplasia; atherosclerosis; restenosis;  
 glomerulonephritis; hypertension; obstructive bladder disease;  
 tubulosclerosis; asthma; interstitial tubular disease; human; gene;  
 patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1921)

AUTHORS Miano, J.M., Streb, J.W., Chen, J.

TITLE New retinoid-inducible serine carboxypeptidase proteins and nucleic  
 acids, useful for detecting or treating vascular diseases, e.g.  
 vascular hyperplasia, atherosclerosis, asthma, glomerulonephritis,  
 hypertension -

JOURNAL Patent: WO200268599-A2; Filing Date: 22-FEB-2002; 2002WO-US05560;  
 Publication Date: 06-SEP-2002; Priority: 22-FEB-2001;  
 2001US-271183P. 23-MAY-2001; 2001US-293097P; Assignee: (UYRP ) UNIV  
 ROCHESTER; Cross Reference: WPI; 2002-713371/77. P-PSDB; ABB99215;  
 Patent Format: Disclosure; Page 21-22; 129pp; English.

COMMENT The invention relates to a novel mammalian retinoid-inducible serine  
 carboxypeptidase (RISC) protein or polypeptide. The proteins of the  
 invention have antiarteriosclerotic, antihypertensive, nephrotropic,  
 antiasthmatic, and vasotropic activity. The polynucleotides of the  
 invention may have a use in gene therapy. The retinoid-inducible  
 serine carboxypeptidase protein and the nucleic acid molecule are  
 useful in detecting, preventing or treating vascular diseases or  
 disorders, e.g. vascular hyperplasia, atherosclerosis, restenosis,  
 glomerulonephritis, hypertension, obstructive bladder disease,  
 tubulosclerosis, asthma or interstitial tubular disease, in  
 inhibiting smooth muscle cell growth and inhibiting the activity of  
 extracellular regulated kinase. The transgenic animal is useful in  
 screening and identifying agents that induce or suppress the  
 function of the retinoid-inducible genes. The sequence encodes the  
 human RISC of the invention.

FEATURES Location/Qualifiers

5'UTR 1..32

/\*tag= b

CDS 33..1391

/\*tag= a

/product= "RISC"

3'UTR 1391..1921

/\*tag= c

BASE COUNT 502 a 412 c 486 g 521 t

ORIGIN

P\_ABV77921 Hypoxia-induced protein coding sequence #35. 921 bp,  
DNA, PAT 12-NOV-2002

ACCESSION P\_ABV77921

KEYWORDS Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclampsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss; human; gene; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1921)

AUTHORS White,J., Mundy,C.R., Ward,N.R., Krige,D., Kingsman,S.M.,  
Harris,R.A. Rayner,W.N.

TITLE Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially regulated gene -

JOURNAL Patent: WO200246465-A2; Filing Date: 10-DEC-2001; 2001WO-GB05458; Publication Date: 13-JUN-2002; Priority: 08-DEC-2000; 2000GB-0030076. 08-FEB-2001; 2001GB-0003156. 25-OCT-2001; 2001GB-0025666; Assignee: (OXFO-) OXFORD BIOMEDICA UK LTD; Cross Reference: WPI; 2002-627238/67; Patent Format: Claim 23; Page 306; 538pp; English.

COMMENT The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV77873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss.

FEATURES Location/Qualifiers

BASE COUNT 502 a 413 c 487 g 519 t

ORIGIN

AF282618 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)  
mRNA, complete cds. 1921 bp, mRNA, linear, PRI 27-SEP-2000

ACCESSION AF282618

VERSION AF282618.1 GI:10312168

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



REFERENCE 1 (bases 1 to 1921)  
 AUTHORS Cho, J.-J. and Baik, H.-H.  
 TITLE Cloning of novel serine carboxypeptidase precursor  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1921)  
 AUTHORS Cho, J.-J. and Baik, H.-H.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JUN-2000) Microbiology, Kyung Hee University, Hoeki  
 1, Seoul 130-701, Korea  
 FEATURES Location/Qualifiers  
 source 1..1921  
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 gene 1..1921  
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 CDS 33..1391  
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 /product="serine carboxypeptidase 1 precursor protein"  
 /protein\_id="AAG16692.1"  
 /db\_xref="GI:10312169"  
 BASE COUNT 502 a 413 c 487 g 519 t  
 ORIGIN

NM\_021626 Homo sapiens likely homolog of rat and mouse retinoid-inducible  
 serine carboxypeptidase (RISC), mRNA. 1921 bp,  
 mRNA, linear, PRI 23-DEC-2002  
 ACCESSION NM\_021626  
 VERSION NM\_021626.1 GI:11055991  
 KEYWORDS REFSEQ; RISC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1921)  
 AUTHORS Chen, J., Streb, J.W., Maltby, K.M., Kitchen, C.M. and Miano, J.M.  
 TITLE Cloning of a novel retinoid-inducible serine carboxypeptidase from  
 vascular smooth muscle cells  
 JOURNAL J. Biol. Chem. 276 (36), 34175-34181 (2001)  
 MEDLINE 21424023  
 PUBMED 11447226  
 REFERENCE 2 (bases 1 to 1921)  
 AUTHORS Cho, J.-J. and Baik, H.-H.  
 TITLE Cloning of novel serine carboxypeptidase precursor  
 JOURNAL Unpublished  
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final  
 NCBI review. The reference sequence was derived from AF282618.1.  
 FEATURES Location/Qualifiers  
 source 1..1921  
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 /db\_xref="taxon:9606"  
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 gene 1..1921  
 /gene="RISC"  
 /note="synonym: HSCP1"

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CDS          /db_xref="LocusID:59342"
             33..1391
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             /product="serine carboxypeptidase 1 precursor protein"
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             /db_xref="GI:11055992"
             /db_xref="LocusID:59342"
misc_feature  156..1370
             /gene="RISC"
             /note="serine_carbpept; Region: Serine carboxypeptidase"
             /db_xref="CDD:pfam00450"
misc_feature  171..1379
             /gene="RISC"
             /note="COG2939; Region: Carboxypeptidase C (cathepsin A)
             [Amino acid transport and metabolism]"
             /db_xref="CDD:COG2939"
BASE COUNT   502 a    413 c    487 g    519 t
ORIGIN

```

P\_AA15579 Human cDNA sequence SEQ ID NO:13881. 641 bp, cDNA, PAT 26-JUN-2001

ACCESSION P\_AA15579

KEYWORDS Human; primer; detection; diagnosis; antisense therapy; gene therapy; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1641)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J. Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.

TITLE Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -

JOURNAL Patent: EP1074617-A2; Filing Date: 28-JUL-2000; 2000EP-0116126; Publication Date: 07-FEB-2001; Priority: 29-JUL-1999; 99JP-0248036. 27-AUG-1999; 99JP-0300253. 11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767. 09-JUN-2000; 2000JP-0241899; Assignee: (HELI-) HELIX RES INST; Cross Reference: WPI; 2001-318749/34; Patent Format: Claim 8; SEQ ID 13881; 2537pp + CD ROM; English.

COMMENT The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the

abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

FEATURES                      Location/Qualifiers  
 BASE COUNT            412 a       364 c       451 g       414 t  
 ORIGIN

P\_ABV28721 Human prostate expression marker cDNA 28712. 973 bp,  
 cDNA, PAT 16-SEP-2002

ACCESSION P\_ABV28721

KEYWORDS Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic  
 marker; pharmacogenomic marker; gene; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1973)

AUTHORS Schlegel, R., Endege, W.O., Monahan, J.E.

TITLE Novel isolated nucleic acid molecule associated with cancerous state  
 of prostate cells and correlating with presence of prostate cancer,  
 useful for detecting presence of prostate cancer, stage of prostate  
 cancer -

JOURNAL Patent: WO200160860-A2; Filing Date: 20-FEB-2001; 2001WO-US05171;  
 Publication Date: 23-AUG-2001; Priority: 17-FEB-2000;  
 2000US-183319P. 16-MAR-2000; 2000US-189862P. 25-MAY-2000;  
 2000US-207454P. 09-JUN-2000; 2000US-211314P. 18-JUL-2000;  
 2000US-219007P. 13-DEC-2000; 2000US-255281P; Assignee: (MILL-)  
 MILLENNIUM PREDICTIVE MEDICINE INC; Cross Reference: WPI;  
 2001-662795/76; Patent Format: Claim 1; Page 6030-6031; 11750pp;  
 English.

COMMENT The invention relates to an isolated nucleic acid molecule (I)  
 comprising a nucleotide sequence given in Tables 1-9  
 (ABV00010-ABV62213) of the specification or its complement. (I) is  
 useful for: (a) assessing whether a patient is afflicted with  
 prostate cancer; (b) monitoring the progression of prostate cancer  
 in a patient; (c) assessing the efficacy of a test compound to  
 inhibit prostate cancer in a patient; (d) assessing the efficacy of  
 a therapy for inhibiting prostate cancer in a patient; (e) selecting  
 a composition for inhibiting prostate cancer in a patient; (f)  
 assessing the prostate cell carcinogenic potential of a compound;  
 (g) determining whether prostate cancer has metastasized in a  
 patient; (h) assessing the aggressiveness or indolence of prostate  
 cancer in a patient; (I) is also useful as a pharmacodynamic or  
 pharmacogenomic marker.

FEATURES                      Location/Qualifiers  
 BASE COUNT            519 a       418 c       495 g       522 t       19 others  
 ORIGIN

AK027373 Homo sapiens cDNA FLJ14467 fis, clone MAMMA1000672, weakly similar  
 to VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.16.-). 1641 bp,  
 mRNA, linear, PRI 01-AUG-2002

ACCESSION AK027373

VERSION AK027373.1 GI:14042005

KEYWORDS oligo capping; fis (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,  
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,  
Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,  
Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,  
Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,  
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,  
Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.

TITLE NEDO human cDNA sequencing project

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1641)

AUTHORS Isogai,T. and Otsuki,T.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,  
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

COMMENT NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing:  
Research Association for Biotechnology; cDNA library construction,  
5'- & 3'-end one pass sequencing and clone selection: Helix  
Research Institute (supported by Japan Key Technology Center etc.)  
and Department of Virology, Institute of Medical Science,  
University of Tokyo.

FEATURES Location/Qualifiers

source

1..1641

/organism="Homo sapiens"

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/clone="MAMMA1000672"

/tissue\_type="mammary gland"

/clone\_lib="MAMMA1"

/note="cloning vector: pME18SFL3"

CDS

27..1385

/note="unnamed protein product"

/codon\_start=1

/protein\_id="BAB55069.1"

/db\_xref="GI:14042006"

BASE COUNT 412 a 364 c 451 g 414 t

ORIGIN

BD157571 Primer for synthesizing full-length cDNA and use thereof. 1641 bp,  
DNA, linear, PAT 17-JAN-2003

ACCESSION BD157571

VERSION BD157571.1 GI:27863329

KEYWORDS JP 2002191363-A/12414.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1641)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,  
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 12414 09-JUL-2002;

HELIX RESEARCH INSTITUTE

COMMENT OS Homo sapiens (human)

PN JP 2002191363-A/12414

PD 09-JUL-2002  
PF 28-JUL-2000 JP 2000280990  
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU  
PI SAITO,  
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,  
PI KEIICHI NAGAI, TETSUJI OTSUKI  
PC

C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC  
10,

PC C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC  
Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers  
FT CDS (27)..(1382).

FEATURES Location/Qualifiers  
source 1..1641  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 412 a 364 c 451 g 414 t  
ORIGIN

-- P\_AAH72787 Human cervical cancer marker nucleic acid 4061. 977 bp,  
cDNA, PAT 19-SEP-2001

ACCESSION P\_AAH72787

KEYWORDS Cervical cancer; cytostatic; pre-malignant condition; gene therapy;  
patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1977)

AUTHORS Schlegel, R., Deeds, J., Berger, A., Zhao, X.

TITLE New isolated nucleic acid for diagnosing and treating cervical  
cancer and for assessing and detecting compounds for treating the  
cancer -

JOURNAL Patent: WO200142467-A2; Filing Date: 08-DEC-2000; 2000WO-US33312;  
Publication Date: 14-JUN-2001; Priority: 08-DEC-1999;  
99US-0169681. 21-DEC-1999; 99US-0171350. 14-MAR-2000;  
2000US-0189315. 12-MAY-2000; 2000US-0203791. 09-JUN-2000;  
2000US-0210600. 21-JUL-2000; 2000US-0220114; Assignee: (MILL-)  
MILLENNIUM PREDICTIVE MEDICINE INC; Cross Reference: WPI;  
2001-375006/39; Patent Format: Claim 1; Page 853; 1051pp; English.

COMMENT The invention relates to novel genes (AAH68727-AAH73383) associated  
with cervical cancer with cytostatic activity. The nucleic acids and  
encoded polypeptides are useful: to assess if a patient is afflicted  
with cervical cancer or has a pre-malignant condition; to monitor  
the progression of cervical cancer or a premalignant condition in a  
patient; and to select and/or assess the efficacy of a compound or  
therapy for inhibiting cervical cancer in a patient. The nucleic  
acids may also be useful for gene therapy.

FEATURES Location/Qualifiers  
BASE COUNT 520 a 421 c 496 g 521 t 19 others  
ORIGIN

— AX188369 Sequence 4064 from Patent WO0142467. 1977 bp,  
DNA, linear, PAT 06-AUG-2001

ACCESSION AX188369

VERSION AX188369.1 GI:15139842

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Schlegel,R., Deeds,J., Berger,A. and Zhao,X.

TITLE Genes, compositions, kits, and methods for identification,  
assessment, prevention, and therapy of cervical cancer

JOURNAL Patent: WO 0142467-A 4064 14-JUN-2001;  
Millennium Predictive Medicine, Inc. (US)

FEATURES Location/Qualifiers

source 1..1977

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 520 a 421 c 496 g 521 t 19 others

ORIGIN

P\_AAD12590 Human protein having hydrophobic domain encoding cDNA clone HP03959.  
897 bp, cDNA, PAT 25-SEP-2001

ACCESSION P\_AAD12590

KEYWORDS Human; hydrophobic domain; gene therapy; nutritional supplement;  
cell proliferation; immunomodulatory; autoimmune disorder;  
antimicrobial; multiple sclerosis; rheumatoid arthritis;  
insulin-dependent diabetes; haematopoiesis; tissue growth activity;  
Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's  
disease; chemotactic; chemokinetic; haemostatic; thrombolytic;  
tumour growth inhibitor; anabolic; contraceptive; antiinfertility;  
antiinflammatory; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1897)

AUTHORS Kato,S., Kimura,T.

TITLE Human proteins with hydrophobic domains and the nucleic acids  
encoding them, useful for preventing diagnosing and treating e.g.  
cancer, Alzheimer's and inflammation -

JOURNAL Patent: WO200149728-A2; Filing Date: 28-DEC-2000; 2000WO-JP09359;  
Publication Date: 12-JUL-2001; Priority: 06-JAN-2000;  
2000JP-0000585. 06-JAN-2000; 2000JP-0000588. 11-JAN-2000;  
2000JP-0002299. 03-FEB-2000; 2000JP-0026862. 03-MAR-2000;  
2000JP-0058367; Assignee: (PROT-) PROTEGENE INC. (SAGA ) SAGAMI CHEM  
RES CENT; Cross Reference: WPI; 2001-418355/44. P-PSDB; AAE06595;  
Patent Format: Claim 4; Page 410-413; 563pp; English.

COMMENT The present sequence is human protein with hydrophobic domain  
encoding cDNA clone HP03959. The polynucleotide and polypeptide of  
the invention may be used in the prevention, diagnosis and treatment  
of diseases associated with inappropriate polypeptide expression.  
The polynucleotides may be used to produce the polypeptide, by  
inserting the nucleic acids into a host cell and culturing the cell  
to express the protein. The polynucleotides and its complementary  
sequences may also be used as DNA probes in diagnostic assays and  
also used in gene therapy. The polypeptides may also be used as  
antigens in the production of antibodies and in assays to identify  
modulators of polypeptide expression and activity. The polypeptides  
and nucleic acids may be used as nutritional supplements, to  
modulate cytokine and cell proliferation activity, to modulate  
immune stimulation or suppression (e.g. for the treatment of  
microbial infections and autoimmune disorders such as multiple  
sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to  
modulate haematopoiesis, to modulate tissue growth activity (e.g.  
for the treatment of Parkinson's disease, Huntington's disease and

Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.

FEATURES                      Location/Qualifiers  
       CDS                      8..1366  
                               /\*tag= a  
                               /product= "Human protein having hydrophobic domain"  
                               /note= "CDS is specifically is claimed in claim 3"  
       sig\_peptide            8..88  
                               /\*tag= b  
       mat\_peptide            89..1363  
                               /\*tag= c  
                               /product= "Mature human protein with hydrophobic domain"  
 BASE COUNT            499 a      406 c      477 g      515 t  
 ORIGIN

AX191563      Sequence 85 from Patent WO0149728. 1897 bp,  
                               DNA, linear, PAT 15-AUG-2001

ACCESSION      AX191563

VERSION        AX191563.1    GI:15209749

KEYWORDS       .

SOURCE        Homo sapiens (human)

ORGANISM       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1

AUTHORS        Kato,S. and Kimura,T.

TITLE           Human proteins having hydrophobic domains and dnas encoding these  
                               proteins

JOURNAL        Patent: WO 0149728-A 85 12-JUL-2001;

Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)

FEATURES                      Location/Qualifiers

      source                    1..1897  
                               /organism="Homo sapiens"  
                               /db\_xref="taxon:9606"  
       CDS                       8..1366  
                               /note="unnamed protein product"  
                               /codon\_start=1  
                               /protein\_id="CAC51169.1"  
                               /db\_xref="GI:15209750"

BASE COUNT            499 a      406 c      477 g      515 t  
 ORIGIN

AF113214      Homo sapiens MSTP034 mRNA, complete cds. 1902 bp,  
                               mRNA, linear, HTC 12-APR-2002

ACCESSION      AF113214

VERSION        AF113214.1    GI:11640575

KEYWORDS       HTC.

SOURCE        Homo sapiens (human)

ORGANISM       Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE      1    (bases 1 to 1902)

AUTHORS        Liu,B., Liu,Y.Q., Wang,X.Y., Zhao,B., Sheng,H., Zhao,X.W., Liu,S.,  
                               Xu,Y.Y., Ye,J., Song,L., Gao,Y., Zhang,C.L., Zhang,J., Wei,Y.J.,  
                               Cao,H.Q., Zhao,Y., Liu,L.S., Ding,J.F., Gao,R.L., Wu,Q.Y.,

Qiang,B.Q., Yuan,J.G., Liew,C.C., Zhao,M.S. and Hui,R.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-DEC-1998) Molecular Medical Center for Cardiovascular  
 Disease, Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu,  
 Beijing 100037, P.R. China  
 FEATURES Location/Qualifiers  
 source 1..1902  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /tissue\_type="aorta"  
 CDS 129..1337  
 /codon\_start=1  
 /product="MSTP034"  
 /protein\_id="AAG39285.1"  
 /db\_xref="GI:11640576"  
 BASE COUNT 517 a 400 c 475 g 510 t  
 ORIGIN

P\_AAC75884 Human ORFX ORF1439 polynucleotide sequence SEQ ID NO:2877. 921 bp,  
 cDNA, PAT 08-FEB-2001

ACCESSION P\_AAC75884

KEYWORDS Human; open reading frame; ORFX; detection; cytostatic;  
 hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic;  
 neuroprotective; anticonvulsant; osteopathic; antiarthritic;  
 immunosuppressant; cardiant; immunostimulant; thrombolytic;  
 coagulant; vasotropic; antidiabetic; hypotensive; dermatological;  
 immunosuppressive; antiinflammatory; antiviral; antibacterial;  
 antifungal; antirheumatic; antithyroid; antianaemic; gene therapy;  
 cancer; proliferative disorder; hypertension; neurodegenerative  
 disorder; osteoarthritis; graft vs host disease; cardiovascular  
 disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol  
 ester storage; systemic lupus erythematosus; infection; severe  
 combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 bone damage; cartilage damage; antiinflammatory disease;  
 coagulation; thrombosis; contraceptive; patent; GENESEQ patentdb.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1921)

AUTHORS Shimkets,R.A., Leach,M.

TITLE Novel nucleic acids and peptides derived from open reading frame X,  
 useful for treating e.g. cancers, proliferative disorders,  
 neurodegenerative disorders and cardiovascular disease -

JOURNAL Patent: WO200058473-A2; Filing Date: 31-MAR-2000; 2000WO-US08621;  
 Publication Date: 05-OCT-2000; Priority: 31-MAR-1999;  
 99US-0127607. 02-APR-1999; 99US-0127636. 05-APR-1999;  
 99US-0127728. 30-MAR-2000; 2000US-0540763; Assignee: (CURA-) CURAGEN  
 CORP; Cross Reference: WPI; 2000-602362/57. P-PSDB; AAB41675; Patent  
 Format: Claim 5; Page 2113-2115; 5507pp; English.

COMMENT AAC74446 to AAC77606 encode the proteins given in AAB40237 to  
 AAB43397, which represent the human ORFX open reading frames 1 to  
 3161. The ORFX sequences have activities such as: cytostatic;  
 hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic;  
 neuroprotective; osteopathic; anticonvulsant; antiarthritic;  
 immunosuppressant; immunostimulant; cardiant; thrombolytic;  
 coagulant; vasotropic; antidiabetic; hypotensive; dermatological;  
 immunosuppressive; antiinflammatory; antibacterial; antiviral;  
 antifungal; antirheumatic; antithyroid; and antianaemic. The



FEATURES	Location/Qualifiers				
BASE COUNT	506 a	411 c	485 g	518 t	1 others
ORIGIN					

COMMENT The invention relates to an isolated human protease nucleic acid molecule comprising a nucleotide sequence of 546 base pairs, one of 268 fully defined in the specification. Also disclosed are production of an isolated polypeptide encoded by the nucleic acid, comprising introducing the nucleic acid into a host cell and culturing under conditions to express the protein from the nucleic acid, use of an antibody to detect the encoded protein in a sample and to modulate its in vivo activity, identifying agents that bind to the protein and identification of a polynucleotide agent that modulates the expression of the nucleic acid or its complement (i.e. gene therapy). The nucleic acid can be used to identify an agent that modulates the expression or activity of the nucleic acid, and can be used to isolate the protein. The nucleic acid can be used in diagnostic assays for determining nucleic acid expression as well as activity in the context of a biological sample (e.g., blood, serum, cells, tissue) to determine whether an individual has a disease or disorder, or is at risk of developing a disease or disorder, associated with aberrant expression or activity of the nucleic acid. The nucleic acid can be used to detect mutations in protease genes and gene expression products such as mRNA. The nucleic acid can be

used as hybridisation probes to detect naturally-occurring genetic mutations in a protease gene. The nucleic acid can be used in drug screening methods to identify agonists and antagonists that can be used to diagnose and treat such protease mediated disorders e.g., proliferative, differentiative, developmental or haematopoietic disorders. The nucleic acid can be used as probes, primers, in biological assays, to determine patterns of gene expression, to design ribozymes and to construct transgenic animals. The present sequence represents one of the 268 disclosed human G-protein-coupled protease cDNA sequences.

FEATURES                      Location/Qualifiers  
 BASE COUNT                525 a       418 c       493 g       524 t  
 ORIGIN

— P AAH89926 Human bone marrow cDNA, SEQ ID NO: 57. 940 bp,  
 cDNA, PAT 01-OCT-2001

ACCESSION    P AAH89926

KEYWORDS     Human; bone marrow; antiinflammatory; cytostatic; neuroprotective;  
 antiviral; antibacterial; antifungal; anti-HIV; haemostatic;  
 immunosuppressive; gene therapy; cytokine cell proliferation; cell  
 differentiation modulator; immune disorder; infection; cancer; human  
 immunodeficiency virus; HIV; autoimmune disorder; haemophilia;  
 patent; GENESEQ patentdb.

SOURCE       Homo sapiens.

ORGANISM      Homo sapiens.

REFERENCE     1 (bases 1 to 1940)

✓ AUTHORS     Ford,J.E., Boyle,B.J., Tang,Y.T., Liu,C., Asundi,V., Chen,R.,  
 Ma,Y. Ren,F., Wang,J., Werhman,T., Xu,C., Xue,A.J., Yang,Y.,  
 Zhang,J. Zhao,Q.A., Zhou,P., Drmanac,R.T.

TITLE          Novel bone-marrow-expressed polynucleotides and polypeptides, useful  
 for treating e.g. cancer and immune deficiency disorders -

JOURNAL       Patent: WO200153453-A2; Filing Date: 23-DEC-2000; 2000WO-US34960;  
 Publication Date: 26-JUL-2001; Priority: 21-JAN-2000;  
 2000US-0488725. 25-APR-2000; 2000US-0552317. 09-JUL-2000;  
 2000US-0598042. 19-JUL-2000; 2000US-0620312. 03-AUG-2000;  
 2000US-0653450. 14-SEP-2000; 2000US-0662191. 19-OCT-2000;  
 2000US-0693036. 30-NOV-2000; 2000US-0250583; Assignee: (HYSE-) HYSEQ  
 INC; Cross Reference: WPI; 2001-488707/53. P-PSDB; AAM00807; Patent  
 Format: Claim 1; Page 244-245; 648pp; English.

COMMENT       The present sequence is one of 251 novel human polynucleotides  
 expressed in the bone marrow. The polynucleotide and the polypeptide  
 encoded by it are useful in the treatment of various immune  
 deficiencies and disorders. The deficiencies and disorders may be  
 genetic, may be caused by a viral (e.g. HIV), bacterial or fungal  
 infection, or may result from an autoimmune disorder, a coagulation  
 disorder (e.g. haemophilia), inhibition of tumour cell  
 proliferation, suppression of an inflammatory response or treatment  
 of a nervous system disorder such as Alzheimer's disease. Detection  
 of the presence or increased expression of the polynucleotide or the  
 protein it encodes is useful for the diagnosis and/or prognosis of  
 one or more types of cancer. The polynucleotide and polypeptide can  
 be used as nutritional sources or supplements and in the screening  
 of chemical compounds as potential drugs.

FEATURES                      Location/Qualifiers  
 BASE COUNT                537 a       410 c       469 g       524 t  
 ORIGIN

— AX191553       Sequence 75 from Patent WO0149728. 1359 bp,

DNA, linear, PAT 15-AUG-2001  
 ACCESSION AX191553  
 VERSION AX191553.1 GI:15209735  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Kato, S. and Kimura, T.  
 TITLE Human proteins having hydrophobic domains and dnas encoding these  
 proteins  
 JOURNAL Patent: WO 0149728-A 75 12-JUL-2001;  
 Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP)  
 FEATURES Location/Qualifiers  
 source 1..1359  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 337 a 318 c 375 g 329 t  
 ORIGIN

Tue Apr 1 16:16:15 2003 [BLASTP 2.2.2 [Jan-08-2002], NCBI]  
/home/glinda/vf/Legal/byeung/pl.DNA40370 (452 aa)  
/home/glinda/vf/Legal/byeung/pl.DNA40370  
Database: day (2,655,410 seqs, 680,241,903 aa) Mar 24, 2003 2:54 PM  
Locus list: hum (596,938 seqs, 114,350,192 aa)  
Matrix: BLOSUM62, T: 11, A: 40, X1: 16, X2: 38, X3: 64, S1: 41, S2: 75, eval:  
10.  
Gap Penalties: Existence: 11, Extension: 1

Sequences producing High-scoring Segment Pairs:				Score	Match	Pct	E-val
1	P_ABB84842	Human PRO302 protein sequence SEQ ID NO:52		2382	452	100	0.0
2	P_ABB95448	Human angiogenesis related protein PRO302		2382	452	100	0.0
3	P_ABP65102	Hypoxia-induced protein #28 - Homo sapiens		2382	452	100	0.0
4	P_ABB99215	Human retinoid inducible serine carboxypep		2382	452	100	0.0
5	P_AAB80255	Human PRO302 protein - Homo sapiens.		2382	452	100	0.0
6	P_AAB20341	Human PRO302 - Homo sapiens.		2382	452	100	0.0
7	P_AAB93913	Human protein sequence SEQ ID NO:13882 - H		2382	452	100	0.0
8	P_AAE06595	Human protein having hydrophobic domain, H		2382	452	100	0.0
9	P_AAY88378	PRO302, vitellogenic carboxypeptidase homo		2382	452	100	0.0
10	P_AAY13387	protein PRO302 - Homo sapiens.		2382	452	100	0.0
11	P_AAY05768	Human PRO216 (vitellogenic carboxypeptidas		2382	452	100	0.0
12	CAC51169.1	unnamed protein product - Homo sapiens		2382	452	100	0.0
13	AAG16692.1	serine carboxypeptidase 1 precursor protei		2382	452	100	0.0
14	BAB55069.1	unnamed protein product - Homo sapiens		2382	452	100	0.0
15	NP_067639.1	serine carboxypeptidase 1 precursor protei		2382	452	100	0.0
16	RISC_HUMAN	Retinoid-inducible serine carboxypeptidase		2382	452	100	0.0
17	P_AAU96225	Human secreted protein, SEQ ID No 127 - Ho		2372	451	100	0.0
18	P_AAB41675	Human ORFX ORF1439 polypeptide sequence SE		2306	439	97	0.0
19	AAG39285.1	MSTP034 - Homo sapiens		2116	402	100	0.0

>1 P\_ABB84842 Human PRO302 protein sequence SEQ ID NO:52 - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****		
P_ABB84842	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****		
DNA40370	61	SKCNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****		
P_ABB84842	61	SKCNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****		
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
*****		
P_ABB84842	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
*****		
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****		
P_ABB84842	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****		
DNA40370	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****		
P_ABB84842	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****		
DNA40370	301	VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****		
P_ABB84842	301	VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****		

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSFVKS YKN  
\*\*\*\*\*  
P\_ABB84842 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSFVKS YKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE  
\*\*\*\*\*  
P\_ABB84842 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>2 P\_ABB95448 Human angiogenesis related protein PRO302 SEQ ID NO: 52 - Homo  
(452 aa) [1 seg]  
Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN  
\*\*\*\*\*  
P\_ABB95448 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT  
\*\*\*\*\*  
P\_ABB95448 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL  
\*\*\*\*\*  
P\_ABB95448 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA  
\*\*\*\*\*  
P\_ABB95448 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH  
\*\*\*\*\*  
P\_ABB95448 241 VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG  
\*\*\*\*\*  
P\_ABB95448 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSFVKS YKN  
\*\*\*\*\*  
P\_ABB95448 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSFVKS YKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE  
\*\*\*\*\*  
P\_ABB95448 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>3 P\_ABP65102 Hypoxia-induced protein #28 - Homo sapiens. (452 aa) [1 seg]  
Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN  
\*\*\*\*\*  
P\_ABP65102 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT  
\*\*\*\*\*  
P\_ABP65102 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGT

```

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
P_ABP65102 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_ABP65102 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGlyREATeLWGKAEMiIEQNTDGVNFYNIltKSTPTSTMESSLEFtQSHLVCLCQRH
*****
P_ABP65102 241 VNKGlyREATeLWGKAEMiIEQNTDGVNFYNIltKSTPTSTMESSLEFtQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKkLKiIPeDQSWGGQATNVFVNMEEDFMKpViSiVDeLLEAG
*****
P_ABP65102 301 VRHLQRDALSQLMNGPIRKkLKiIPeDQSWGGQATNVFVNMEEDFMKpViSiVDeLLEAG

DNA40370 361 INVTvYNGQLDLiVDtMGQeAWVRKLkWPeLPKfSQLKwKALySDPKSLEtSAFVKsYKn
*****
P_ABP65102 361 INVTvYNGQLDLiVDtMGQeAWVRKLkWPeLPKfSQLKwKALySDPKSLEtSAFVKsYKn

DNA40370 421 LAFYWILKAGHMVPSDQGDmALKmMRLVtQQE
*****
P_ABP65102 421 LAFYWILKAGHMVPSDQGDmALKmMRLVtQQE

>4 P_ABB99215 Human retinoid inducible serine carboxypeptidase - Homo (452 aa)
[1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_ABB99215 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_ABB99215 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
*****
P_ABB99215 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_ABB99215 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGlyREATeLWGKAEMiIEQNTDGVNFYNIltKSTPTSTMESSLEFtQSHLVCLCQRH
*****
P_ABB99215 241 VNKGlyREATeLWGKAEMiIEQNTDGVNFYNIltKSTPTSTMESSLEFtQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKkLKiIPeDQSWGGQATNVFVNMEEDFMKpViSiVDeLLEAG
*****
P_ABB99215 301 VRHLQRDALSQLMNGPIRKkLKiIPeDQSWGGQATNVFVNMEEDFMKpViSiVDeLLEAG

DNA40370 361 INVTvYNGQLDLiVDtMGQeAWVRKLkWPeLPKfSQLKwKALySDPKSLEtSAFVKsYKn
*****
P_ABB99215 361 INVTvYNGQLDLiVDtMGQeAWVRKLkWPeLPKfSQLKwKALySDPKSLEtSAFVKsYKn

DNA40370 421 LAFYWILKAGHMVPSDQGDmALKmMRLVtQQE

```

\*\*\*\*\*  
P\_ABB99215 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

>5 P\_AAB80255 Human PRO302 protein - Homo sapiens. (452 aa) [1 seg]  
Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB80255 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB80255 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
*****
P_AAB80255 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB80255 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB80255 241 VNKGlyREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB80255 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKS YKN
*****
P_AAB80255 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKS YKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAB80255 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
```

>6 P\_AAB20341 Human PRO302 - Homo sapiens. (452 aa) [1 seg]  
Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB20341 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB20341 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
*****
P_AAB20341 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB20341 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
```

```

DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB20341 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB20341 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS YKN
*****
P_AAB20341 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS YKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMA LKMMRLVTQQE
*****
P_AAB20341 421 LAFYWILKAGHMVPSDQGDMA LKMMRLVTQQE

```

>7 P\_AAB93913 Human protein sequence SEQ ID NO:13882 - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB93913 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB93913 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAB93913 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB93913 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB93913 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB93913 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS YKN
*****
P_AAB93913 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKS YKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMA LKMMRLVTQQE
*****
P_AAB93913 421 LAFYWILKAGHMVPSDQGDMA LKMMRLVTQQE

```

>8 P\_AAE06595 Human protein having hydrophobic domain, HP03959 - Homo (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452



DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
		*****
P_AAE06595	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
		*****
P_AAE06595	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
		*****
P_AAE06595	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
		*****
P_AAE06595	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
		*****
P_AAE06595	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370	301	VRHLQRDALSQLMNGPIRKKLKI IPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
		*****
P_AAE06595	301	VRHLQRDALSQLMNGPIRKKLKI IPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPEL PKFSQLKWALYSDPKSLETSAFVKSYKN
		*****
P_AAE06595	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPEL PKFSQLKWALYSDPKSLETSAFVKSYKN
DNA40370	421	LAFYWILKAGHMPSPDQGD MALKMMRLVTQQE
		*****
P_AAE06595	421	LAFYWILKAGHMPSPDQGD MALKMMRLVTQQE

>9 P\_AAY88378 PRO302, vitellogenic carboxypeptidase homologue amino acid  
sequence - Homo sapiens. (452 aa) [1 seg]  
Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
		*****
P_AAY88378	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
		*****
P_AAY88378	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
		*****
P_AAY88378	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
		*****
P_AAY88378	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
		*****
P_AAY88378	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

```

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY88378 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY88378 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMPVSDQGDMALKMMRLVTQQE
*****
P_AAY88378 421 LAFYWILKAGHMPVSDQGDMALKMMRLVTQQE

```

>10 P\_AAY13387 protein PRO302 - Homo sapiens. (452 aa) [1 seg]  
Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAY13387 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAY13387 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAY13387 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY13387 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAY13387 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY13387 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY13387 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMPVSDQGDMALKMMRLVTQQE
*****
P_AAY13387 421 LAFYWILKAGHMPVSDQGDMALKMMRLVTQQE

```

>11 P\_AAY05768 Human PRO216 (vitellogenic carboxypeptidase homologue) - Homo  
(452 aa) [1 seg]  
Score = 2382 (922 bits), Expect = 0.0  
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAY05768 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

```

```

*****
P_AAY05768 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAY05768 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY05768 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGlyREATeLWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAY05768 241 VNKGlyREATeLWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY05768 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPelpKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY05768 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPelpKFSQLKWKALYSDPKSLETSAFVKSYKN
DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAY05768 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>12 CAC51169.1 unnamed protein product - Homo sapiens (452 aa) [1 seg]  
 Score = 2382 (922 bits), Expect = 0.0  
 Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
CAC51169.1 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
CAC51169.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
CAC51169.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
CAC51169.1 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGlyREATeLWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
CAC51169.1 241 VNKGlyREATeLWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
CAC51169.1 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPelpKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
CAC51169.1 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPelpKFSQLKWKALYSDPKSLETSAFVKSYKN

```

DNA40370 421 LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE  
 \*\*\*\*\*  
 CAC51169.1 421 LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE

>13 AAG16692.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN  
 \*\*\*\*\*  
 AAG16692.1 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT  
 \*\*\*\*\*  
 AAG16692.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL  
 \*\*\*\*\*  
 AAG16692.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA  
 \*\*\*\*\*  
 AAG16692.1 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH  
 \*\*\*\*\*  
 AAG16692.1 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG  
 \*\*\*\*\*  
 AAG16692.1 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPEL PKFSQLKWALYSDPKSLETSAFVKSYKN  
 \*\*\*\*\*  
 AAG16692.1 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPEL PKFSQLKWALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE  
 \*\*\*\*\*  
 AAG16692.1 421 LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE

>14 BAB55069.1 unnamed protein product - Homo sapiens (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN  
 \*\*\*\*\*  
 BAB55069.1 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT  
 \*\*\*\*\*  
 BAB55069.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL  
 \*\*\*\*\*  
 BAB55069.1 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****		
BAB55069.1	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****		
BAB55069.1	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370	301	VRHLQRDALSQLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****		
BAB55069.1	301	VRHLQRDALSQLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****		
BAB55069.1	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
DNA40370	421	LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE
*****		
BAB55069.1	421	LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE

>15 NP\_067639.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****		
NP_067639.1	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
*****		
NP_067639.1	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSLKPRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
*****		
NP_067639.1	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****		
NP_067639.1	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****		
NP_067639.1	241	VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370	301	VRHLQRDALSQLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****		
NP_067639.1	301	VRHLQRDALSQLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****		
NP_067639.1	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKSYKN
DNA40370	421	LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE
*****		
NP_067639.1	421	LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE

>16 RISC\_HUMAN Retinoid-inducible serine carboxypeptidase precursor  
 /pid=AAG16692.1 - homo sapiens (452 aa) [1 seg]  
 Score = 2382 (922 bits), Expect = 0.0  
 Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
		*****
RISC_HUMAN	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
		*****
RISC_HUMAN	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
		*****
RISC_HUMAN	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
		*****
RISC_HUMAN	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370	241	VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
		*****
RISC_HUMAN	241	VNKGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370	301	VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
		*****
RISC_HUMAN	301	VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKS YKN
		*****
RISC_HUMAN	361	INVTVYNGQLDLIVDTMGQEAWVRKLKWPPELKFSQLKWKALYSDPKSLETSAFVKS YKN
DNA40370	421	LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE
		*****
RISC_HUMAN	421	LAFYWILKAGHMPVPSDQGDMAKMMRLVTQQE

>17 P\_AAU96225 Human secreted protein, SEQ ID No 127 - Homo sapiens. (452 aa) [1 seg]  
 Score = 2372 (918 bits), Expect = 0.0  
 Identities = 451/452 (99%), Positives = 451/452 (99%), at 1,1-452,452

DNA40370	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
		*****
P_AAU96225	1	MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
		*****
P_AAU96225	61	SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKLRKTTWLQAASLLFVDNPVGT
DNA40370	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
		*****
P_AAU96225	121	GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLEL
DNA40370	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
		*****
P_AAU96225	181	YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

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DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAU96225 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAU96225 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAU96225 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELKFSQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAU96225 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>18 P\_AAB41675 Human ORFX ORF1439 polypeptide sequence SEQ ID NO:2878 - Homo (451 aa) [1 seg]  
Score = 2306 (892 bits), Expect = 0.0  
Identities = 439/452 (97%), Positives = 444/452 (98%), Gaps = 1/452 (0%), at 1,1-452,451

```

DNA40370 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
P_AAB41675 1 MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATT

DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB41675 61 PART-SELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAB41675 120 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370 181 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB41675 180 YKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAB41675 240 VNKGLYREATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB41675 300 VRHLQRDALSQLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVIDIVDTLLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLKWPELKFSQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAB41675 360 VNVTVYNGQLDLIVDTIGQEAWVRKLKWPELSRFNQLKWKALYSDPKSLETSAFVKSYKN

DNA40370 421 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
*****
P_AAB41675 420 LAFYWILKAGHMVPSDQGDMAKMMRLVTQQE

```

>19 AAG39285.1 MSTP034 - Homo sapiens (402 aa) [1 seg]  
Score = 2116 (819 bits), Expect = 0.0  
Identities = 402/402 (100%), Positives = 402/402 (100%), at 51,1-452,402

DNA40370	51	MFWWLYYATNSCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAAS
		*****
AAG39285.1	1	MFWWLYYATNSCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAAS
DNA40370	111	LLFVDNPVGTGFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGG
		*****
AAG39285.1	61	LLFVDNPVGTGFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGG
DNA40370	171	KMAAGIGLELYKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEV
		*****
AAG39285.1	121	KMAAGIGLELYKAIQRGTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEV
DNA40370	231	SKVAEQVLNAVNGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESLEFTQ
		*****
AAG39285.1	181	SKVAEQVLNAVNGLYREATELWGKAEMIEQNTDGVNFYNILTKSTPTSTMESLEFTQ
DNA40370	291	SHLVCLCQRHVRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVI
		*****
AAG39285.1	241	SHLVCLCQRHVRHLQRDALSQLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVI
DNA40370	351	SIVDELLEAGINVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLE
		*****
AAG39285.1	301	SIVDELLEAGINVTVYNGQLDLIVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLE
DNA40370	411	TSAFVKSYKNLAFYWILKAGHMVPSDQGDMAKMMRLVTQQE
		*****
AAG39285.1	361	TSAFVKSYKNLAFYWILKAGHMVPSDQGDMAKMMRLVTQQE



Dayhoff Protein Database (Rel 75, Feb 2003)

P\_ABB84842 Human PRO302 protein sequence SEQ ID NO:52 - Homo sapiens.

Length: 452 aa

Accession: P\_ABB84842;

Species: Homo sapiens.

Keywords: Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; patent; GENESEQ patentdb.

Patent number: WO200200690-A2.

Publication date: 03-JAN-2002.

Filing date: 20-JUN-2001; 2001WO-US19692.

Priority: 23-JUN-2000; 2000US-213637P. 20-JUL-2000; 2000US-219556P.

25-JUL-2000; 2000US-220624P.30-MAY-2001; 2001WO-US17443.

01-JUN-2001; 2001WO-US17800. plus 32 more dates.

Assignee: (GETH ) GENENTECH INC.

Inventors: Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

Cross reference: WPI; 2002-090516/12. N-PSDB; ABL88097.

Title: One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -

Patent format: Claim 11; Fig 52; 565pp; English.

Comment: ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.

Database: GENESEQ patent database.

P\_ABB95448 Human angiogenesis related protein PRO302 SEQ ID NO: 52 - Homo sapiens.

Length: 452 aa

Accession: P\_ABB95448;

Species: Homo sapiens.

Keywords: Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; patent; GENESEQ patentdb.

Patent number: WO200208284-A2.  
Publication date: 31-JAN-2002.  
Filing date: 09-JUL-2001; 2001WO-US21735.  
Priority: 20-JUL-2000; 2000US-219556P. 25-JUL-2000; 2000US-220624P.  
25-JUL-2000; 2000US-220664P. 20-JUN-2001; 2001WO-US19692.  
28-JUN-2001; 2001WO-US00000. plus 34 more dates.  
Assignee: (GETH ) GENENTECH INC. (BAKE/) BAKER K P. (FERR/) FERRARA N.  
(GERB/) GERBER H. (GERR/) GERRITSEN M E. (GODD/) GODDARD A. (GODO/) GODOWSKI P J. (GURN/) GURNEY A L. (HILL/) HILLAN K J. (MARS/) MARSTERS S A. (PANJ/) PAN J. (PAON/) PAONI N F. (STEP/) STEPHAN J F. (WATA/) WATANABE C K. (WILL/) WILLIAMS P M. (WOOD/) WOOD W I.  
Inventors: Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF; Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
Cross reference: WPI; 2002-171999/22. N-PSDB; ABL95586.  
Title: One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -  
Patent format: Claim 11; Fig 52; 567pp; English.  
Comment: The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a PRO protein of the invention.  
Database: GENESEQ patent database.

P\_ABP65102 Hypoxia-induced protein #28 - Homo sapiens.  
Length: 452 aa  
Accession: P\_ABP65102;  
Species: Homo sapiens.  
Keywords: Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclampsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss; human; patent; GENESEQ patentdb.  
Patent number: WO200246465-A2.  
Publication date: 13-JUN-2002.  
Filing date: 10-DEC-2001; 2001WO-GB05458.  
Priority: 08-DEC-2000; 2000GB-0030076. 08-FEB-2001; 2001GB-0003156.  
25-OCT-2001; 2001GB-0025666.  
Assignee: (OXFO-) OXFORD BIOMEDICA UK LTD.  
Inventors: White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA; Rayner WN;  
Cross reference: WPI; 2002-627238/67.  
Title: Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially regulated gene -  
Patent format: Claim 13; Page 305; 538pp; English.  
Comment: The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological

condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV77873-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclampsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss.

Database: GENESEQ patent database.

P\_ABB99215 Human retinoid inducible serine carboxypeptidase - Homo sapiens.

Length: 452 aa

Accession: P\_ABB99215;

Species: Homo sapiens.

Keywords: Serine carboxypeptidase; mammalian; RISC; antihypertensive; retinoid-inducible serine carboxypeptidase; antiarteriosclerotic; nephrotropic; antiasthmatic; vasotropic; gene therapy; vascular disease; vascular hyperplasia; atherosclerosis; restenosis; glomerulonephritis; hypertension; obstructive bladder disease; tubulosclerosis; asthma; interstitial tubular disease; human; patent; GENESEQ patentdb.

Patent number: WO200268599-A2.

Publication date: 06-SEP-2002.

Filing date: 22-FEB-2002; 2002WO-US05560.

Priority: 22-FEB-2001; 2001US-271183P. 23-MAY-2001; 2001US-293097P.

Assignee: (UYRP ) UNIV ROCHESTER.

Inventors: Miano JM, Streb JW, Chen J;

Cross reference: WPI; 2002-713371/77. N-PSDB; ABV72656.

Title: New retinoid-inducible serine carboxypeptidase proteins and nucleic acids, useful for detecting or treating vascular diseases, e.g. vascular hyperplasia, atherosclerosis, asthma, glomerulonephritis, hypertension -

Patent format: Claim 39; Page 20-21; 129pp; English.

Comment: The invention relates to a novel mammalian retinoid-inducible serine carboxypeptidase (RISC) protein or polypeptide. The proteins of the invention have antiarteriosclerotic, antihypertensive, nephrotropic, antiasthmatic, and vasotropic activity. The polynucleotides of the invention may have a use in gene therapy. The retinoid-inducible serine carboxypeptidase protein and the nucleic acid molecule are useful in detecting, preventing or treating vascular diseases or disorders, e.g. vascular hyperplasia, atherosclerosis, restenosis, glomerulonephritis, hypertension, obstructive bladder disease, tubulosclerosis, asthma or interstitial tubular disease, in inhibiting smooth muscle cell growth and inhibiting the activity of extracellular regulated kinase. The transgenic animal is useful in screening and identifying agents that induce or suppress the function of the retinoid-inducible genes. The sequence represents the human RISC of

the invention.  
73-82/Binding-site  
/label= Serine\_carboxypeptidase\_binding\_site/  
163-170/Domain  
/label= First\_catalytic\_domain/  
365-373/Domain  
/label= Second\_catalytic\_domain/  
421-437/Domain  
/label= Third\_catalytic\_domain/  
Database: GENESEQ patent database.

P\_AAB80255 Human PRO302 protein - Homo sapiens.

Length: 452 aa

Accession: P\_AAB80255;

Species: Homo sapiens.

Keywords: Human; PRO; dermatological; antipsoriatic; cytostatic;  
antiinflammatory; antiparkinsonian nootropic; neuroprotective;  
vulnerary; cardiant; antiangiogenic; vasotropic; antiasthmatic;  
antirheumatic; cancer; antiarthritic; antiinfertility;  
antidiabetic; antiviral; diabetes; ophthalmological; gene therapy;  
skin disease; gastrointestinal disorder; ischaemia; inflammation;  
patent; GENESEQ patentdb.

Patent number: WO200104311-A1.

Publication date: 18-JAN-2001.

Filing date: 22-FEB-2000; 2000WO-US04414.

Priority: 07-JUL-1999; 99US-0143048. 26-JUL-1999; 99US-0145698.

28-JUL-1999; 99US-0146222. 08-SEP-1999; 99WO-US20594. 13-SEP-1999;  
99WO-US20944. 15-SEP-1999; 99WO-US21090. 15-SEP-1999; 99WO-US21547.  
05-OCT-1999; 99WO-US23089. 29-NOV-1999; 99WO-US28214. 30-NOV-1999;  
99WO-US28313. 16-DEC-1999; 99WO-US30095. 20-DEC-1999; 99WO-US30911.  
20-DEC-1999; 99WO-US30999. 05-JAN-2000; 99WO-US00219.

Assignee: (GETH ) GENENTECH INC.

Inventors: Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;  
Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;  
Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ; Mather  
JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D; Williams PM, Wood  
WI;

Cross reference: WPI; 2001-081051/09. N-PSDB; AAF72416.

Title: Sixty one nucleic acids encoding PRO polypeptides which are useful  
in the treatment of skin diseases (e.g. psoriasis), cancers (e.g.  
lung squamous cell carcinoma) and neurodegenerative diseases (e.g.  
Alzheimer's disease) -

Patent format: Claim 1; Fig 90; 393pp; English.

Comment: The present sequence is one of sixty one novel secreted and  
transmembrane PRO polypeptides. The PRO polypeptides are useful for  
treating skin diseases (e.g. psoriasis), cancers (e.g. lung  
squamous cell carcinoma), gastrointestinal disorders (e.g.  
enterocolitis), neurodegenerative diseases (e.g. Alzheimer's  
disease, Parkinson's disease), wound repair, cardiovascular  
disorders (e.g. endometrial bleeding angiogenesis, ischaemias such  
as coronary ischaemia, atherosclerosis), inflammatory disorders  
(e.g. asthma, rheumatoid arthritis, multiple sclerosis),  
infertility, AIDS and diabetes and retinal disorders such as  
retinitis pigmentosum. The PRO nucleic acids have applications in  
molecular biology, including use as hybridization probes, and in  
chromosome and gene mapping.

Database: GENESEQ patent database.

P\_AAB20341 Human PRO302 - Homo sapiens.

Length: 452 aa

Accession: P\_AAB20341;

Species: Homo sapiens.

Keywords: PRO302; vitellogenic carboxypeptidase homologue; human; angiogenesis; cardiovascularisation; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy; macular degeneration; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive; antirheumatic; antiarthritic; antiinflammatory; vulnerary; antitumour; diagnosis; therapy; patent; GENESEQ patentdb.

Patent number: WO200119987-A1.

Publication date: 22-MAR-2001.

Filing date: 29-NOV-1999; 99WO-US28214.

Priority: 13-SEP-1999; 99WO-US20944. 15-SEP-1999; 99WO-US21090.

Assignee: (GETH ) GENENTECH INC.

Inventors: Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan KJ; Williams PM, Wood WI;

Cross reference: WPI; 2001-235264/24. N-PSDB; AAF30502.

Title: Composition comprising a PRO230, PRO216 or PRO302 polypeptide, agonist or antagonist for promoting or inhibiting angiogenesis and/or cardiovascularisation in mammals -

Patent format: Claim 55; Fig 6; 141pp; English.

Comment: The present sequence is that of human PRO302, a novel secreted protein (51 kDa, pI 5.74) that is a homologue of vitellogenic carboxypeptidase. The sequence is predicted from isolated PRO302 cDNA (see AAF30502). PRO302 is 1 of 3 novel PRO polypeptides of the invention. PRO230, PRO216 and PRO302 polynucleotides and polypeptides, recombinant retroviral particles, ex vivo producer cells, expression vectors, host cells, and methods of recombinant production are provided, as well as antibodies, agonists and antagonists. The polynucleotides, polypeptides, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration (all claimed), atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarction, thrombophlebitis and lymphangitis. The polypeptides, agonists and antagonists are also used in claimed methods of stimulating or inhibiting endothelial cell growth.

1-25/Peptide

/label= Signal\_peptide/

26-452/Protein

/label= Mature\_protein/

64-68/Modified-site

/note= Asn is N-glycosylated/

126-130/Modified-site

/note= Asn is N-glycosylated/

362-366/Modified-site

/note= Asn is N-glycosylated/

204-208/Modified-site

/note= O-phosphorylated by casein kinase II/

220-224/Modified-site

/note= O-phosphorylated by casein kinase II/

280-284/Modified-site

/note= O-phosphorylated by casein kinase II/

284-288/Modified-site

/note= O-phosphorylated by casein kinase II/

351-355/Modified-site

/note= O-phosphorylated by casein kinase II/  
449-453/Modified-site  
/note= O-phosphorylated by casein kinase II/  
101-105/Modified-site  
/note= O-phosphorylated by cAMP- and cGMP-/  
dependent protein kinase/  
22-28/Modified-site  
/note= N-myristoylated/  
76-82/Modified-site  
/note= N-myristoylated/  
79-85/Modified-site  
/note= N-myristoylated/  
80-86/Modified-site  
/note= N-myristoylated/  
119-125/Modified-site  
/note= N-myristoylated/  
168-175/Modified-site  
/note= N-myristoylated/  
187-193/Modified-site  
/note= N-myristoylated/  
195-201/Modified-site  
/note= N-myristoylated/  
331-337/Modified-site  
/note= N-myristoylated/  
332-338/Modified-site  
/note= N-myristoylated/  
360-366/Modified-site  
/note= N-myristoylated/  
Database: GENESEQ patent database.

P\_AAB93913 Human protein sequence SEQ ID NO:13882 - Homo sapiens.  
Length: 452 aa  
Accession: P\_AAB93913;  
Species: Homo sapiens.  
Keywords: Human; primer; detection; diagnosis; antisense therapy; gene  
therapy; patent; GENESEQ patentdb.  
Patent number: EP1074617-A2.  
Publication date: 07-FEB-2001.  
Filing date: 28-JUL-2000; 2000EP-0116126.  
Priority: 29-JUL-1999; 99JP-0248036. 27-AUG-1999; 99JP-0300253.  
11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767.  
09-JUN-2000; 2000JP-0241899.  
Assignee: (HELI-) HELIX RES INST.  
Inventors: Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
Cross reference: WPI; 2001-318749/34.  
Title: Primer sets for synthesizing polynucleotides, particularly the 5602  
full-length cDNAs defined in the specification, and for the  
detection and/or diagnosis of the abnormality of the proteins  
encoded by the full-length cDNAs -  
Patent format: Claim 8; SEQ ID 13882; 2537pp + CD ROM; English.  
Comment: The present invention describes primer sets for synthesizing 5602  
full-length cDNAs defined in the specification. Where a primer set  
comprises: (a) an oligo-dT primer and an oligonucleotide  
complementary to the complementary strand of a polynucleotide which  
comprises one of the 5602 nucleotide sequences defined in the  
specification, where the oligonucleotide comprises at least 15  
nucleotides; or (b) a combination of an oligonucleotide comprising

a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Database: GENESEQ patent database.

P\_AAE06595 Human protein having hydrophobic domain, HP03959 - Homo sapiens.

Length: 452 aa

Accession: P\_AAE06595;

Species: Homo sapiens.

Keywords: Human; hydrophobic domain; gene therapy; nutritional supplement; cell proliferation; immunomodulatory; autoimmune disorder; antimicrobial; multiple sclerosis; rheumatoid arthritis; insulin-dependent diabetes; haematopoiesis; tissue growth activity; Parkinson's disease; cytostatic; Huntington's disease; Alzheimer's disease; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour growth inhibitor; anabolic; contraceptive; antiinfertility; antiinflammatory; patent; GENESEQ patentdb.

Patent number: WO200149728-A2.

Publication date: 12-JUL-2001.

Filing date: 28-DEC-2000; 2000WO-JP09359.

Priority: 06-JAN-2000; 2000JP-0000585. 06-JAN-2000; 2000JP-0000588.

11-JAN-2000; 2000JP-0002299. 03-FEB-2000; 2000JP-0026862.

03-MAR-2000; 2000JP-0058367.

Assignee: (PROT-) PROTEGENE INC. (SAGA ) SAGAMI CHEM RES CENT.

Inventors: Kato S, Kimura T;

Cross reference: WPI; 2001-418355/44. N-PSDB; AAD12590.

Title: Human proteins with hydrophobic domains and the nucleic acids encoding them, useful for preventing diagnosing and treating e.g. cancer, Alzheimer's and inflammation -

Patent format: Claim 1; Page 368-370; 563pp; English.

Comment: The present sequence is human protein with hydrophobic domain, HP03959. The polynucleotide and polypeptide of the invention may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The polynucleotides may be used to produce the polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The polynucleotides and its complementary sequences may also be used as DNA probes in diagnostic assays and also used in gene therapy. The polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators of polypeptide expression and activity. The polypeptides and nucleic acids may be used as nutritional supplements, to modulate cytokine and cell proliferation activity, to modulate

immune stimulation or suppression (e.g. for the treatment of microbial infections and autoimmune disorders such as multiple sclerosis, rheumatoid arthritis and insulin-dependent diabetes), to modulate haematopoiesis, to modulate tissue growth activity (e.g. for the treatment of Parkinson's disease, Huntington's disease and Alzheimer's disease), to modulate activin and inhibin activity (e.g. for controlling fertility), to modulate chemotactic and chemokinetic activity, to modulate haemostatic and thrombolytic activity, to modulate receptor ligand activity, to modulate inflammation and to inhibit tumour growth.

1-27/Peptide

/label= Signal\_peptide/

28-452/Protein

/note= Mature human protein with hydrophobic domain/

Database: GENESEQ patent database.

P\_AAY88378 PRO302, vitellogenic carboxypeptidase homologue amino acid sequence - Homo sapiens.

Length: 452 aa

Accession: P\_AAY88378;

Species: Homo sapiens.

Keywords: Human; PRO302; Vitellogenic carboxypeptidase; cardiant; angiogenic; cytostatic; ophthalmic; antiproliferative activity; cardiovascular; endothelial; angiogenic disorder; cardiac hypertrophy; trauma; cancer; myocardial infarction; age-related macular degeneration; patent; GENESEQ patentdb.

Patent number: WO200015792-A2.

Publication date: 23-MAR-2000.

Filing date: 13-SEP-1999; 99WO-US20944.

Priority: 14-SEP-1998; 98US-0100262. 14-SEP-1998; 98WO-US19177.

Assignee: (GETH ) GENENTECH INC.

Inventors: Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan KJ; Williams PM, Wood WI;

Cross reference: WPI; 2000-271431/23. N-PSDB; AAA13199.

Title: A composition comprising PRO230, PRO216 or PRO302 polypeptides, agonists or antagonists useful for promotion or inhibition of cardiovascularisation, angiogenesis or endothelialisation in mammals -

Patent format: Example 3; Fig 6; 135pp; English.

Comment: This sequence represents the human PRO302 amino acid sequence.

PRO302 is a human vitellogenic carboxypeptidase homologue. The invention relates to a composition comprising a PRO230 (tubulointerstitial nephritis antigen homologue), PRO216 (osteomodulin/fibromodulin homologue) or PRO302 (vitellogenic carboxypeptidase homologue) polypeptide, or an agonist or antagonist of these. Also included in the invention is a method for preparing the composition, agonists and antagonists of PRO230, PRO216 or PRO302, and antibodies that bind to a PRO230, PRO216 or PRO302 polypeptides. The composition of the invention has cardiant, angiogenic, cytostatic, ophthalmic, and antiproliferative activity. Analysis of the level of expression of a gene encoding a PRO230, PRO216 or PRO302 polypeptide or detecting the presence/absence of the polypeptide is useful for diagnosis of cardiovascular, endothelial or angiogenic disorders in mammals. Anti-PRO230, PRO216 or PRO302 antibodies are useful in these diagnostic methods. The PRO230, PRO216 or PRO302 polypeptides (and their coding sequences), agonists and antagonists are useful for treatment of cardiovascular, endothelial or angiogenic disorders, especially



cardiac hypertrophy (especially characterized by presence of an elevated level of PGF-2alpha), trauma or cancer, myocardial infarction or age-related macular degeneration. In particular, PRO216, an agonist of PRO216, an antagonist of PRO230, PRO216 or PR302 or an anti-PRO216 antibody is useful for inhibition of endothelial cell growth in a mammal. Endothelial cell growth can be stimulated by administration of PRO230, a PRO230 agonist or antagonist or an anti-PRO230 antibody. Additionally, an anti-PRO302 antibody can inhibit angiogenesis induced by PRO302 in a mammal.

Database: GENESEQ patent database.

P\_AAY13387 Amino acid sequence of protein PRO302 - Homo sapiens.

Length: 452 aa

Accession: P\_AAY13387;

Species: Homo sapiens.

Keywords: Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair; patent; GENESEQ patentdb.

Patent number: WO9914328-A2.

Publication date: 25-MAR-1999.

Filing date: 16-SEP-1998; 98WO-US19330.

Priority: 25-NOV-1997; 97US-0066840. 17-SEP-1997; 97US-0059113.

17-SEP-1997; 97US-0059115. 24-NOV-1997; 97US-0066511. 24-NOV-1997; 97US-0066453. plus 47 more dates.

Assignee: (GETH ) GENENTECH INC.

Inventors: Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

Cross reference: WPI; 1999-229533/19. N-PSDB; AAX52258.

Title: New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration

Patent format: Claim 12; Fig 90; 320pp; English.

Comment: AAY13344-403 represent secreted and transmembrane human proteins.

The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.

Database: GENESEQ patent database.

P\_AAY05768 Human PRO216 (vitellogenic carboxypeptidase homologue) - Homo sapiens.

Length: 452 aa

Accession: P\_AAY05768;

Species: Homo sapiens.

Keywords: PRO302; vitellogenic carboxypeptidase; human; angiogenesis; cardiovascularisation; wound healing; cancer; atherosclerosis; cardiac hypertrophy; myocardial infarction; antiangiogenic; antitumour; tissue regeneration; pulmonary fibrosis; neurological disease; macular degeneration; diagnosis; therapy; patent; GENESEQ patentdb.

Patent number: WO9914234-A2.

Publication date: 25-MAR-1999.

Filing date: 14-SEP-1998; 98WO-US19177.

Priority: 24-NOV-1997; 97US-0066772. 17-SEP-1997; 97US-0059117. 27-OCT-1997; 97US-0063329.

Assignee: (GETH ) GENENTECH INC.

Inventors: Fong S, Gerritsen ME, Goddard A, Gurney AL, Hillan K; Williams PM, Woodwi;

Cross reference: WPI; 1999-254381/21. N-PSDB; AAX25445.

Title: Composition containing human polypeptides with anti-angiogenic activity

Patent format: Example 1; Fig 9; 102pp; English.

Comment: The present sequence represents human PRO302, identified as a vitellogenic carboxypeptidase homologue. The sequence was deduced from cDNA clone UNQ265 (DNA40370-1217, ATCC 209485, see AAX25445). Compositions containing PRO302, PRO216 (human osteomodulin, see AAY05767) or PRO230 in admixture with a carrier are claimed. The compositions are used to treat or prevent a wide range of cardiovascular, endothelial and angiogenic disorders (claimed), specifically cardiac hypertrophy (especially where associated with elevated levels of prostaglandin F2 alpha or induced by myocardial infarction), trauma (wounds, burns, or tissue regeneration more generally, including neurological disease), and cancer. Antagonists may be used similarly, also to treat age-related macular degeneration (or other angiogenic retinal disorders) and to prevent excessive growth of connective tissue during wound healing or in pulmonary fibrosis.

1-25/Peptide

/note= signal peptide/

26-452/Protein

/note= mature protein/

64/Modified-site

/note= N-glycosylated/

126/Modified-site

/note= N-glycosylated/

362/Modified-site

/note= N-glycosylated/

Database: GENESEQ patent database.

CAC51169.1 unnamed protein product - Homo sapiens

Length: 452 aa

Species: Homo sapiens (human)

Kato, S. and Kimura, T., Patent: WO 0149728-A 85 12-JUL-2001; Protegene Inc. (JP) ; SAGAMI CHEMICAL RESEARCH CENTER (JP) Title: Human proteins having hydrophobic domains and dnas encoding these proteins

Locus: AX191563  
Accession: AX191563  
Cross-references: taxon:9606; GI:15209750; AX191563\_1  
Database: GBTRANS

AAG16692.1 serine carboxypeptidase 1 precursor protein - Homo sapiens  
Length: 452 aa  
Species: Homo sapiens (human)  
Cho, J.-J. and Baik, H.-H., Submitted (26-JUN-2000) Microbiology, Kyung Hee  
University, Hoeki 1, Seoul 130-701, Korea Title: Direct Submission  
Gene: HSCP1  
Locus: AF282618  
Accession: AF282618  
Cross-references: taxon:9606; GI:10312169; AF282618\_1  
Database: GBTRANS

BAB55069.1 unnamed protein product - Homo sapiens  
Length: 452 aa  
Species: Homo sapiens (human)  
Isogai, T. and Otsuki, T., Submitted (10-MAY-2001) Takao Isogai, Helix  
Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu,  
Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp,  
Tel: 81-438-52-3975, Fax: 81-438-52-3986) Title: Direct Submission  
Locus: AK027373  
Accession: AK027373  
Cross-references: taxon:9606; GI:14042006; AK027373\_1  
Database: GBTRANS

RISC\_HUMAN Retinoid-inducible serine carboxypeptidase precursor  
/pid=AAG16692.1 - homo sapiens  
Length: 452 aa  
Species: Homo sapiens (Human).  
Accession: Q9HB40; EMBL; AF282618; AAG16692.1. EMBL; AK027373; BAB55069.1.  
MEROPS; S10.013; -. InterPro; IPR000379; Ser\_estrs\_site. InterPro;  
IPR001563; Serine\_carbpept. Pfam; PF00450; serine\_carbpept; 1.  
PRINTS; PR00724; CRBOXYPTASEC. ProDom; PD001189; Serine\_carbpept;  
2. PROSITE; PS00131; CARBOXYPEPT\_SER\_SER; 1. PROSITE; PS00560;  
CARBOXYPEPT\_SER\_HIS; FALSE\_NEG.  
Cho J.-J., Baik H.-H., Submitted (jun-2000) to the EMBL/genbank/ddbj  
databases. (ref. 1: sequence from n.a.) Title: "Cloning of novel  
serine carboxypeptidase precursor."  
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa  
T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M.,  
Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi  
M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
Ninomiya K., Iwayanagi T., Submitted (may-2001) to the  
EMBL/genbank/ddbj databases. (ref. 2: sequence from n.a.  
tissue=mammary gland;) Title: "NEDO human cDNA sequencing project."  
Keywords: hydrolase; carboxypeptidase; glycoprotein; signal.  
Taxid: tx:9606  
Gene name: RISC OR SCP1.  
1-26/Domain: Signal Potential.  
27-452/Domain: Retinoid-Inducible Serine Carboxypeptidase.  
167/Site: Act\_site By Similarity.  
371/Site: Act\_site By Similarity.  
431/Site: Act\_site By Similarity.

64/Site: Carbohyd N-Linked (glcnac...) (potential).  
126/Site: Carbohyd N-Linked (glcnac...) (potential).  
362/Site: Carbohyd N-Linked (glcnac...) (potential).  
Database: Swissprot (SPROT), Release 40 (Jan 11, 2003)

P\_AAU96225 Human secreted protein, SEQ ID No 127 - Homo sapiens.  
Length: 452 aa

Accession: P\_AAU96225;

Species: Homo sapiens.

Keywords: Human; secreted protein; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; breast; liver; ischaemia; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; corneal infection; wound healing; ocular disorder; skin aging; sunburn; epithelial cell proliferation; organ transplantation; food additive; food storage; patent; GENESEQ patentdb.

Patent number: WO200224721-A1.

Publication date: 28-MAR-2002.

Filing date: 09-JAN-2001; 2001WO-US00544.

Priority: 20-SEP-2000; 2000US-234211P.

Assignee: (HUMA-) HUMAN GENOME SCI INC.

Inventors: Komatsoulis GA, Baker KP, Rosen CA, Birse CE, Soppet DR, Olsen HS; Ni J, Fiscella M, Moore PA, Wei P, Ebner R, Duan DR, Shi Y; Choi GH;

Cross reference: WPI; 2002-330012/36.

Title: Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition -

Patent format: Disclosure; Page 13; 562pp; English.

Comment: The invention relates to an isolated nucleic acid molecule (I) encoding a human secreted protein (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to (II) can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAU96165-AAU96237 represent human secreted protein sequences and related sequences used in expression of the secreted proteins as described in examples of the invention.

Database: GENESEQ patent database.

P\_AAB41675 Human ORFX ORF1439 polypeptide sequence SEQ ID NO:2878 - Homo sapiens.

Length: 451 aa

Accession: P\_AAB41675;

Species: Homo sapiens.

Keywords: Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; patent; GENESEQ patentdb.

Patent number: WO200058473-A2.

Publication date: 05-OCT-2000.

Filing date: 31-MAR-2000; 2000WO-US08621.

Priority: 31-MAR-1999; 99US-0127607. 02-APR-1999; 99US-0127636.

05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763.

Assignee: (CURA-) CURAGEN CORP.

Inventors: Shimkets RA, Leach M;

Cross reference: WPI; 2000-602362/57. N-PSDB; AAC75884.

Title: Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Patent format: Claim 11; Page 2115-2116; 5507pp; English.

Comment: AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.

Database: GENESEQ patent database.

AAG39285.1 MSTP034 - Homo sapiens

Length: 402 aa

Species: Homo sapiens (human)

Liu,B., Liu,Y.Q., Wang,X.Y., Zhao,B., Sheng,H., Zhao,X.W., Liu,S., Xu,Y.Y.,  
Ye,J., Song,L., Gao,Y., Zhang,C.L., Zhang,J., Wei,Y.J., Cao,H.Q.,  
Zhao,Y., Liu,L.S., Ding,J.F., Gao,R.L., Wu,Q.Y., Qiang,B.Q.,  
Yuan,J.G., Liew,C.C., Zhao,M.S. and Hui,R.T., Submitted  
(15-DEC-1998) Molecular Medical Center for Cardiovascular Disease,  
Cardiovascular Institute, CAMS & PUMC, 167, Bei Li Shi Lu, Beijing  
100037, P.R. China Title: Direct Submission

Locus: AF113214

Accession: AF113214

Cross-references: taxon:9606; GI:11640576; AF113214\_1

Database: GBTRANS